

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 11, 2006, 09:30:12 ; Search time 50 seconds  
(without alignments)  
765.018 Million cell updates/sec

Title: US-10-727-619-2

Perfect score: 2381

Sequence: 1 MSALLLLALLGFLPLPGVQ.....WGVLALPALMWGVCPSC 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /EMC Celerra\_SID83/ptodata/2/iaa/5 COMB.pcp.\*
  - 2: /EMC Celerra\_SID83/ptodata/2/iaa/6 COMB.pcp.\*
  - 3: /EMC Celerra\_SID83/ptodata/2/iaa/7 COMB.pcp.\*
  - 4: /EMC Celerra\_SID83/ptodata/2/iaa/8 COMB.pcp.\*
  - 5: /EMC Celerra\_SID83/ptodata/2/iaa/9 COMB.pcp.\*
  - 6: /EMC Celerra\_SID83/ptodata/2/iaa/RE COMB.pcp.\*
  - 7: /EMC Celerra\_SID83/ptodata/2/iaa/backfile1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2381	100.0	437	2	US-09-830-189C-2
2	2381	100.0	437	2	US-09-991-181-355
3	2381	100.0	437	2	US-09-990-444-355
4	2381	100.0	437	2	US-10-033-301-16
5	2381	100.0	437	2	US-09-997-333-355
6	2381	100.0	437	2	US-09-992-598-355
7	2381	100.0	437	2	US-10-033-435-16
8	2381	100.0	437	3	US-09-989-735-355
9	2381	100.0	437	3	US-09-989-726-355
10	2381	100.0	437	3	US-09-997-514-355
11	2381	100.0	437	3	US-09-989-728-355
12	2381	100.0	437	3	US-09-997-349-355
13	2381	100.0	437	3	US-09-997-653-355
14	2381	100.0	437	3	US-09-989-293A-355
15	2362	99.2	437	2	US-09-073-569-2
16	438	18.4	81	2	US-09-621-976-4256
17	134.5	5.6	2050	1	US-08-347-594A-2
18	131.5	5.5	819	2	US-10-094-749-1690
19	131.5	5.5	2813	2	US-09-381-261A-1
20	128.5	5.4	212	2	US-09-886-319A-37
21	128	5.4	1404	1	US-08-400-159-2
22	128	5.4	1404	2	US-08-611-729A-2
23	128	5.4	1404	2	US-09-195-524-2
24	127.5	5.4	1964	2	US-09-467-997-1
25	123	5.2	721	2	US-08-872-855-7
26	121.5	5.1	606	3	US-10-029-840A-6

27	121.5	5.1	1253	2	US-08-479-722B-4	Sequence 4, Appli
28	121.5	5.1	1253	2	US-09-592-685-4	Sequence 4, Appli
29	121	5.1	589	2	US-08-991-862-2	Sequence 2, Appli
30	121	5.1	589	2	US-09-813-156-2	Sequence 2, Appli
31	121	5.1	589	2	US-09-456-886-2	Sequence 2, Appli
32	121	5.1	589	2	US-09-824-647-2	Sequence 2, Appli
33	121	5.1	589	2	US-09-880-842-2	Sequence 2, Appli
34	120.5	5.1	2813	2	US-08-896-449A-2	Sequence 2, Appli
35	120.5	5.1	2813	2	US-09-132-652-2	Sequence 2, Appli
36	120.5	5.1	2813	2	US-09-886-900A-2	Sequence 2, Appli
37	120.5	5.1	2813	2	US-09-662-478C-2	Sequence 2, Appli
38	119.5	5.0	833	2	US-09-013-895A-5	Sequence 5, Appli
39	119.5	5.0	833	2	US-09-448-868-5	Sequence 5, Appli
40	119.5	5.0	833	2	US-10-226-296-5	Sequence 5, Appli
41	119	5.0	346	2	US-09-991-181-197	Sequence 197, App
42	119	5.0	346	2	US-09-990-444-197	Sequence 197, App
43	119	5.0	346	2	US-09-997-333-197	Sequence 197, App
44	119	5.0	346	2	US-09-992-598-197	Sequence 197, App
45	119	5.0	346	2	US-09-989-735-197	Sequence 197, App

ALIGNMENTS

RESULT 1

US-09-830-189C-2  
; Sequence 2, Application US/09830189C  
; Patent No. 6686153

; GENERAL INFORMATION:  
; APPLICANT: PAHL, HEIKE

; TITLE OF INVENTION: PRV-1 AND THE USE THEREOF  
; FILE REFERENCE: LEDEP-1

; CURRENT APPLICATION NUMBER: US/09/830,189C

; CURRENT FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: PCT/EP99/07238

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 198 49 044.5

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 2

; LENGTH: 437

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-830-189C-2

Query Match 100.0%; Score 2381; DB 2; Length 437;

Best Local Similarity 100.0%; Pred. No. 8.3e-213;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	LIESGPOVSLVLSKGTCEAKDQBPVTEHRMGPGLSLISYTFVCROQDFCNLVNSLPLW	120
Qy	121	APQPPADPGSLRCPVCLSMEGCLEGTTTETCPKQTHCYDGLRLRGGIFSNLRVQGM	180
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Qy	241	GQVCOETLLLDVGLTSTLVGTGKCVGAGNSOKTTHSAPPGVLVASYTHFSSDLN	300
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QY 421 GLALAPALMWGVVCPSC 437  
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## RESULT 2

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; Sequence 355, Application US/09991181  
; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730F1C53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
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; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
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; PRIOR APPLICATION NUMBER: 60/088021

; PRIOR FILING DATE: 1998-06-04  
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; PRIOR FILING DATE: 1998-06-19

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46 PRIOR FILING DATE: 1998-07-01  
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48 PRIOR FILING DATE: 1998-07-02  
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50 PRIOR FILING DATE: 1998-07-01  
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52 PRIOR FILING DATE: 1998-07-02  
53 PRIOR APPLICATION NUMBER: 60/091626  
54 PRIOR FILING DATE: 1998-07-02  
55 PRIOR APPLICATION NUMBER: 60/091633  
56 PRIOR FILING DATE: 1998-07-02  
57 PRIOR APPLICATION NUMBER: 60/091978  
58 PRIOR FILING DATE: 1998-07-07  
59 PRIOR APPLICATION NUMBER: 60/091982  
60 PRIOR FILING DATE: 1998-07-07  
61 PRIOR APPLICATION NUMBER: 60/092182  
62 PRIOR FILING DATE: 1998-07-09

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Qy 121 APOPPADPGSLRCPVCLSMGCLGTTTETCPKGTTHCYDGLLRGGGIFSNLRVQCGM 180  
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Db 241 GQVCOETLLIDVGLTSTLVGTCGCVGAQNSQKTIHSAPRGVIVASYTHFCSSDLGN 300  
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; Sequence 355, Application US/09990444  
; Patent No. 6930170  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730F1C19  
; CURRENT APPLICATION NUMBER: US/09/990,444  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13





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; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2381; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-213; Indels 0; Gaps 0;
Matches 437; Conservative 0; Mismatches 0;

Qy 1 MSVALLALLGFIPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLM 60
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Db 61 LIESGPQVSLVLSKGCTEAKDQEPRTVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120

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Qy 421 GLALAPALMWGVCPSC 437
Db 421 GLALAPALMWGVCPSC 437
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RESULT 4
US-10-033-301-16
; Sequence 16, Application US/10033301
; Patent No. 6930172
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2930R1C6
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; CURRENT APPLICATION NUMBER: US/10/033,301
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/095,325
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/112,851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,145
; PRIOR FILING DATE: 1998-12-16
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; PRIOR FILING DATE: 2000-12-01
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; SEQ ID NO 16
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-033-301-16
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Best Local Similarity 100.0%; Pred. No. 8.3e-213; Indels 0; Gaps 0;
Matches 437; Conservative 0; Mismatches 0;

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Db 1 MSVALLALLGFIPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLM 60

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RESULT 5  
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; Sequence 355, Application US/09997333  
; Patent No. 6953836  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C27  
; CURRENT APPLICATION NUMBER: US/09/997,333  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
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; Patent No. 6969758  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David  
; APPLICANT: Deanovers, Luc  
; APPLICANT: Feirara, Napoleone  
; APPLICANT: Fogh, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.

;; APPLICANT: Pan, James  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2930R1C5  
;; CURRENT APPLICATION NUMBER: US/10/033,435  
;; CURRENT FILING DATE: 2001-12-27  
;; PRIOR APPLICATION NUMBER: 60/095,325  
;; PRIOR FILING DATE: 1998-08-04  
;; PRIOR APPLICATION NUMBER: 60/112,851  
;; PRIOR FILING DATE: 1998-12-16  
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;; PRIOR FILING DATE: 2000-03-02  
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;; PRIOR FILING DATE: 2000-03-30  
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;; PRIOR APPLICATION NUMBER: PCT/US00/15264  
;; PRIOR FILING DATE: 2000-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: 2000-12-01  
;; NUMBER OF SEQ ID NOS: 38  
;; SEQ ID NO 16  
;; LENGTH: 437  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-033-435-16

Query Match 100.0%; Score 2381; DB 2; Length 437;  
Best Local Similarity 100.0%; Pred. No. 8.3e-213;  
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Db 361 GGLSTKMSIQGCVQAQPSFLLNHTROI GIFSAREKRDVOPPASQHEGGGAEGLESITWGV 420  
QY 421 GLALAPALMWGVCPSC 437  
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RESULT 8

US-09-989-735-355  
; Sequence 355, Application US/09989735  
; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C61  
; CURRENT APPLICATION NUMBER: US/09/989,735  
; CURRENT FILING DATE: 2001-11-19  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
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; Sequence 355, Application US/099899726  
; Patent No. 7018811  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C60  
CURRENT APPLICATION NUMBER: US/09/989,726  
CURRENT FILING DATE: 2001-11-19  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

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US-09-997-514-355

; Sequence 355, Application US/09997514

; Patent No. 7019116  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730F1C46  
; CURRENT APPLICATION NUMBER: US/09/997,514  
; CURRENT FILING DATE: 2001-11-15  
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Db	61	LIESGPQVSLVLSKGCTEAKDQEPVTEHRMGFGLSLISYTFVFCRQEDFCNNLVNSLPLW	120
Qy	121	APQPPADPGSLRCPVCLSMEGCLEGTTTEEICPKGTTTCYDGLLRGGGIFSNLRVQCGM	180
Db	121	APQPPADPGSLRCPVCLSMEGCLEGTTTEEICPKGTTTCYDGLLRGGGIFSNLRVQCGM	180
Qy	181	POPGCNLLNGTOEIGIPVGWMTENCNRKDFLTCHRGTTTMTGHNLAQEPDWTTSNTEMCV	240
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QY 361 GGLSTKMSIQGCVAPQSSFLNHTROIIGIFSAREKRDVOPPASQHEGGGAGLESITW 420  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C37  
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; CURRENT FILING DATE: 2001-11-15

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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 8.3e-213;
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RESULT 13

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; Sequence 355, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Watanabe, Colin K.
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-213;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSVLLLLALLGFIPLPGVQALLCQFGTVQHVWKVSDLPROWTPKNTSCDGLGCGDTLM 60

Qy 61 LIESGPQVSLVLSKGCTEAKDQEPVTEHRMGPGLSLSIYTFVCRQEDFCNNLVNSLPLW 120
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Qy 121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRGGGIFSNLRVQCGM 180
Db 121 APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRGGGIFSNLRVQCGM 180

Qy 181 PQPCNLLNGTOEIGPVGMTECNCRKDFLTCRHGTTIMTGNLAQEPDWTTSNTECEV 240
Db 181 PQPCNLLNGTOEIGPVGMTECNCRKDFLTCRHGTTIMTGNLAQEPDWTTSNTECEV 240

Qy 241 GQVCQETLLLLIDVGLTSLVGTGKSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLGN 300
Db 241 GQVCQETLLLLIDVGLTSLVGTGKSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLGN 300

Qy 301 SASSSSVLLNSLPPQAAAPVPGDRQCPTCVPLGTGTCSSGSPRMTCPRGATHCYDGYIHLG 360
Db 301 SASSSSVLLNSLPPQAAAPVPGDRQCPTCVPLGTGTCSSGSPRMTCPRGATHCYDGYIHLG 360

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QY 421 GLALAPALMWGVCPSC 437  
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; Sequence 355, Application US/09989293A  
; Patent No. 7034136  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C66  
; CURRENT APPLICATION NUMBER: US/09/989,293A  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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RESULT 15  
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; Sequence 2, Application US/09073569  
; Patent No. 6084088  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Grossmann, Angelika  
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,569  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 97-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal

US-09-073-569-2

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Db	61	LIESGQVSLVLSKGTCEAKDQSPRVTHEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW	120		
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Qy	301	SASSSVLLNSLPPQAPVPGDRQCPCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG	360		
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Qy	361	GGSTKMSIQGCVAQSSFLNHTROIQIFSAKRDVQPPASQHEGGGAGLESITWGV	420		
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Db	421	GLALAPALMWVRVCPSC	437		

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Job time : 52 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:48:16 ; Search time 451 Seconds  
(without alignments)  
4612.445 Million cell updates/sec

Title: US-10-727-619-1

Perfect score: 1600

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Scoring table: IDENTITY\_NUC

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Searched: 844069 seqs, 650066433 residues

Total number of hits satisfying chosen parameters: 1688138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	883	55.2	1000	8	US-11-266-748A-295073
4	883	55.2	1000	8	US-11-266-748A-346502
5	874.4	54.6	1000	8	US-11-266-748A-215833
6	874.4	54.6	1000	8	US-11-266-748A-237848
7	627.4	39.2	654	8	US-11-266-748A-2984
8	597.8	37.4	749	8	US-11-266-748A-17659
9	516	32.2	549	8	US-11-266-748A-54407
10	74	4.6	1037	8	US-11-266-748A-368008
11	74	4.6	1037	8	US-11-266-748A-388965
12	74	4.6	1037	8	US-11-266-748A-451387
13	73.2	4.6	1000	8	US-11-266-748A-291309
14	73.2	4.6	1000	8	US-11-266-748A-342738
15	72.4	4.5	1092	8	US-11-266-748A-368007
16	72.4	4.5	1092	8	US-11-266-748A-388964
17	72.4	4.5	1092	8	US-11-266-748A-451386
18	50.4	3.1	1000	8	US-11-266-748A-405181
19	50.4	3.1	1000	8	US-11-266-748A-476227
20	46.4	2.9	533	8	US-11-266-748A-91855
21	46.4	2.9	533	8	US-11-266-748A-144666
22	43.4	2.7	2425	6	US-10-525-647-24
23	41.4	2.6	2271	7	US-11-218-305-9618
24	41	2.6	2084	6	US-10-449-902-9415

25	41	2.6	3707	6	US-10-449-902-14708	Sequence 14708, A
26	40.6	2.5	1778	7	US-11-218-305-1078	Sequence 1078, Ap
27	40.2	2.5	1101	7	US-11-218-305-7614	Sequence 7614, Ap
c 28	39.8	2.5	39536	6	US-10-857-260-27	Sequence 27, Appl
29	39.8	2.5	677	8	US-11-266-748A-81007	Sequence 81007, A
c 30	39.8	2.5	677	8	US-11-266-748A-133818	Sequence 133818, A
31	39.8	2.5	742	6	US-10-449-902-6678	Sequence 6678, Ap
32	39.2	2.5	464	8	US-11-266-748A-300920	Sequence 300920, A
33	39.2	2.5	1296	6	US-10-449-902-19161	Sequence 19161, A
34	39.2	2.5	1693	6	US-10-449-902-15977	Sequence 15977, A
35	39	2.4	1909	6	US-10-449-902-12528	Sequence 12528, A
c 36	38.8	2.4	1707	7	US-11-218-305-22608	Sequence 22608, A
37	38.8	2.4	2390	6	US-10-449-902-22824	Sequence 22824, A
38	38.8	2.4	2457	7	US-11-218-305-16443	Sequence 16443, A
39	38.8	2.4	2501	8	US-11-293-697-1323	Sequence 1323, Ap
40	38.8	2.4	5862	8	US-11-264-243-17	Sequence 17, Appl
41	38.8	2.4	7332	8	US-11-266-748A-28991	Sequence 28991, A
42	38.8	2.4	7693	8	US-11-266-748A-23540	Sequence 23540, A
43	38.8	2.4	9312	8	US-11-264-243-5	Sequence 5, Appli
44	38.8	2.4	9312	8	US-11-266-748A-30265	Sequence 30265, A
45	38.8	2.4	9312	8	US-11-266-748A-56978	Sequence 56978, A

#### ALIGNMENTS

RESULT 1  
US-11-266-748A-369611  
; Sequence 369611, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 369611  
; LENGTH: 986  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (821)..(821)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (833)..(834)  
; OTHER INFORMATION: n is a, c, g, or t  
; US-11-266-748A-369611  
Query Match 58.1%; Score 928.8; DB 8; Length 986;  
Best Local Similarity 96.9%; Pred. No. 1.8e-246;

Matches 956; Conservative 0; Mismatches 30; Indels 1; Gaps 1;  
QY 32 GGTCTAGAGCGCGTATTACTGCTGGCCCTCTCTGGGGTTTCATCTCCACTGCCAGGAGT 91  
DB 1 GGTCTAGAGCGCGGTATTACTGCTGGCCCTCTCTGGGGTTTCATCTCCACTGCCAGGAGT 60  
QY 92 GCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGAAGGTTCGACCTGCC 151  
DB 61 GCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGAAGGTTCGACCTGCC 120  
QY 152 CCGGCAATGACCCCTTAAGAACACAGCTCGGACAGGGGTTGGGTGTCAGACAGCTT 211  
DB 121 CCGGCAATGACCCCTTAAGAACACAGCTCGGACAGGGGTTGGGTGTCAGACAGCTT 180  
QY 212 GATGCTCATTTAGAGCGGACCCCAAGTGAGCTTGGTCTCTCAAGGGTTCGACGAGGC 271  
DB 181 GATGCTCATTTAGAGCGGACCCCAAGTGAGCTTGGTCTCTCAAGGGTTCGACGAGGC 240  
QY 272 CAAGGACCAAGGACCCCGGTCTACTGAGCACCGGATGGGCCCCGGCTCTCTCCCTGATCTC 331  
DB 241 CAAGGACCAAGGACCCCGGTCTACTGAGCACCGGATGGGCCCCGGCTCTCTCCCTGATCTC 300  
QY 332 CTACACCTTCTGTGCGGCGCAGAGACTTCTGCAACAACCTGTTAACTCCCTCCGCT 391  
DB 301 CTACACCTTCTGTGCGGCGCAGAGACTTCTGCAACAACCTGTTAACTCCCTCCGCT 360  
QY 392 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGGGTGCCAGTCTGCTTGTCTAT 451  
DB 361 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGGGTGCCAGTCTGCTTGTCTAT 420  
QY 452 GGAAGGCTGTCTGGAGGGGCAACAGAGAGATCTGCCCAAGGGGACACACACTGTTA 511  
DB 421 GGAAGGCTGTCTGGAGGGGCAACAGAGAGATCTGCCCAAGGGGACACACACTGTTA 480  
QY 512 TGATGGCTCTCAGGCTCAGGGGAGGAGGATCTTCTCAATCTGAGATCCAGGATG 571  
DB 481 TGATGGCTCTCAGGCTCAGGGGAGGAGGATCTTCTCAATCTGAGATCCAGGATG 540  
QY 572 CATGCCCCACAGCTTGCAACCTGCTCAATGGGACACAGGAAATTTGGGCCCTGGGTAT 631  
DB 541 CATGCCCCACAGCTTGCAACCTGCTCAATGGGACACAGGAAATTTGGGCCCTGGGTAT 600  
QY 632 GACTGAGAACTTGGCTCAAGAAAGATTCTTGACCTGTCAATGGGACACCAATATGAC 691  
DB 601 GACTGAGAACTTGGCTCAAGAAAGATTCTTGACCTGTCAATGGGACACCAATATGAC 660  
QY 692 ACACGGAATTTGGCTCAAGAAAGATTCTTGACCTGTCAATGGGACACCAATATGAC 751  
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QY 992 CCCAGGAGACCGGAGTGTCTTACCTG 1018  
DB 960 CCCAGGAGACCGGAGTGTCTTACCTG 986

; Sequence 452990, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 452990  
; LENGTH: 986  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (153)..(154)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (166)..(166)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-452990

Query Match 58.1%; Score 928.8; DB 8; Length 986;  
Best Local Similarity 96.9%; Pred. No. 1.8e-246;  
Matches 956; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 32 GGTCTAGAGCGCGGTATTACTGCTGGCCCTCTCTGGGGTTTCATCTCCACTGCCAGGAGT 91  
DB 986 GGTCTAGAGCGCGGTATTACTGCTGGCCCTCTCTGGGGTTTCATCTCCACTGCCAGGAGT 927  
QY 92 GCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGAAGGTTCGACCTGCC 151  
DB 926 GCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGAAGGTTCGACCTGCC 867  
QY 152 CCGGCAATGACCCCTTAAGAACACAGCTCGGACAGGGGTTGGGTGTCAGACAGCTT 211  
DB 866 CCGGCAATGACCCCTTAAGAACACAGCTCGGACAGGGGTTGGGTGTCAGACAGCTT 807  
QY 212 GATGCTCATTTAGAGCGGACCCCAAGTGAGCTTGGTCTCTCAAGGGTTCGACGAGGC 271  
DB 806 GATGCTCATTTAGAGCGGACCCCAAGTGAGCTTGGTCTCTCAAGGGTTCGACGAGGC 747  
QY 272 CAAGGACCAAGGACCCCGGTCTACTGAGCACCGGATGGGCCCCGGCTCTCTCCCTGATCTC 331  
DB 746 CAAGGACCAAGGACCCCGGTCTACTGAGCACCGGATGGGCCCCGGCTCTCTCCCTGATCTC 687  
QY 332 CTACACCTTCTGTGCGGCGCAGAGACTTCTGCAACAACCTGTTAACTCCCTCCGCT 391  
DB 686 CTACACCTTCTGTGCGGCGCAGAGACTTCTGCAACAACCTGTTAACTCCCTCCGCT 627  
QY 392 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGGGTGCCAGTCTGCTTGTCTAT 451

Db	626	TTGGGCCCCACAGCCCCCAGCAGACCCACAGGATCTCTTGAGGTGCCAGTCTGTGCTGTCTAT	567
Qy	452	GGAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAAGGGGACCAACACTGTTA	511
Db	566	GGAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAAGGGGACCAACACTGTTA	507
Qy	512	TGATGSCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATG	571
Db	506	TGATGSCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATG	447
Qy	572	CATGCCCCACGACGAGGTTCGAACCTGCTCAATGGGACACAGGAAATTTGGGCCCGTGGGTAT	631
Db	446	CATGCCCCACGACGAGTTTGAACCTGCTCAA TGGGACACAGGAAATTTGGGCCCGTGGGTAT	387
Qy	632	GACTGAGAACTGCAATAGAGAAAGATTTTCTGACCTGTCA TCGGGGACCAACCATTTATGAC	691
Db	386	GACTGAGAACTGCGATATGAAAGATTTTCTGACCTGTCA TCGGGGACCAACCATTTATGAC	327
Qy	692	ACACGGAAACTTGGCTCAAGAACCACTGATTTGGACCACATCGAATACCGAGATGTGCGA	751
Db	326	ACACGGAAACTTGGCTCAAGAACCACTGATTTGGACCACATCGAATACCGAGATGTGCGA	267
Qy	752	GGTGGGGCAGGTGTGTTCAGGAGACGCTGCTGCTCATAGATGTAGGATCTCACATCAACCCCT	811
Db	266	AGTGGGGCAGGTGTGTTCAGGAGACGCTGCTGCTCATAGATGTAGGATCTCACATCAACCCCT	207
Qy	812	GGTGGGGCAAAAGCTGTGAGCAGCTGTTGGGGCTCAAAATPCCAGAAGACCAACCATCCA	871
Db	206	GGTGGGGCAAAAGCTGTGAGCAGCTGTTGGGGCTCAAAATPCCAGAAGACCAACCATCCA	147
Qy	872	CTCAGCCCTCCTCGGGGTCTGTGGGCTCTATACCCACTTCTGCTCTCTCGGACCTGTG	931
Db	146	CTCAGCCCTCCTCGGGGTCTGTGGGCTCTATACCCACTTCTGCTCTCTCGGACCTGTG	87
Qy	932	CAATAGTGCACGACGAGCGTGTCTGCTGAACTCCCTCCCTCCTCAAGTCGCCCTGT	991
Db	86	CAATAGTGCACGACGAGCGGTCTGCTGAACTCCCTCCCTCCTCAAGTCGCCCTGT	28
Qy	992	CCGAGAGACCGGACGTGCTTACCTG	1018
Db	27	CCGAGGAGACGGCAGTGTTCCTACCTG	1

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US-11-266-748A-295073  
; Sequence 295073, Application US/11366748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 5815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIORITY FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 295073
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-295073

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Best Local Similarity 94.3%; Pred. No. 8.3e-234;
Matches 938; Conservative 0; Mismatches 55; Indels 2; Gaps 2;

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Db      1    ACACAGGAATTCGGCCCGTGGGTATGACTGTGAACTGCGATATGAAGATGTCTGACC 60

QY      666  TGTTCATCGGGGACACCACTATTGACACACGGAAACTTGGCTCAAGAACCCACTGATTGG 725
Db      61    TGTTCATCGGGGACCACTTGTGAGAGACGAGAAACTTGTGATGAAGAACCCACTGATTGG 120

QY      726  ACCACATCGAATACCGAGATGTCGGAGGTGGCGACGTTGTTCAGGAGACGCTGCTGCTC 785
Db      121    GCCACATCTAATACCGAGACGTCGGAGGTGGGCGACGTTGTTCAGGAGATGCTGCTGCTC 180

QY      786  ATAGATGTAGGACTCACATCAACCTGTGGTGGGACAAAGGCTGCAGCACTGTTCGGGCT 845
Db      181    ATAGATGTAGGACTCATCAACCTGTGGTGGGACCTAAAGCTGCAGCGCTGTTCGGGCT 240

QY      846  CAAAAATCCAGAAAGACCACTCATCTCAGCCCCCTCTGGGGTGTCTTGGGCTCCTAT 905
Db      241    CAAAAATCCAGAAAGACCACTCATCTCAGCCCCCTCTGGGGTGTCTTGGGCTCCTAT 300

QY      906  ACCCACTTCTGCTCCTCGGACCTGTGCAATAGTSCCAGCAGCAGCAGCGTTCTGCTGAAC 965
Db      301    ACCCACTTCTGCTCCTCGGACCTGTGCAATAGTSCCAGCAGCAGCAGCGTTCTGCTGAAC 360

QY      966  TCCTTCCTCTCAAGCTGCCCTGTCCGAGGACCGGCAGTGTCTTACCTGTGTGCAG 1025
Db      361    TCCTTCCTCTCAAGCTGCCCTGTCCGAGGACCGGCAGTGTCTTACCTGTGTGCAG 420

QY      1026  CCCCTTGGAACTGTTCAAGTGTCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCAT 1085
Db      421    CCCCTTGGAACTGTTCAAGTGTCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCAT 480

QY      1086  TGTATTGATGGGTACATTCAATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCAATTCAG 1145
Db      481    TGTATTGATGGGTACATTCAATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCAATTCAG 540

QY      1146  GCGTCGTGGGCCCAACTTCCAGCTTCTTGTGAAACCAACAACAATTCGGGATCTTC 1205
Db      541    GCGTCGTGGGCCCAACTTCCAGCTTCTTGTGAAACCAACAACAATTCGGGATCTTC 600

QY      1206  TCTGCGGCTGAGAAGCGTGTGAGCGCTCCGCTCTCAGCATCAGGAGGATGGGGCT 1265
Db      601    TCTGCTGTGAGAAGGGTGATGAGCGCGCTCTCTGCTCTCAGCATCAGGAGGATGGGGCT 660

QY      1266  GAGGGCTGTGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGG 1325
Db      661    GAGGGCTGTGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGG 720

QY      1326  GGAAGTGGTTGGCCCTTCCTGCTAACTCTATTACCCCAACAATTCACCGCTGTGACC 1385
Db      721    GGAAGCGTTTGGCCCTTCCTGCTAACTCCATTTCCCAACAATTCCTTCAACCGCTGTGACC 780

QY      1386  ACCCACTCAACCTCCCTCTGACCTCATAACTATAGGCTTGGACACAACGATTTCTTT- 1444
Db      781    A-CCACACTCAACCGTCCCTCTGCTGTGTAACCTAATAGGCTTGGACACAACGATTTCTTT 839

QY      1445  CCCATTCTGTGCCATGAATCATCTTCCCAACAACAATCATTCATCTACTCACTCAACA 1504
Db      840    CCCATCCTGTCCATGAATCATCTTCCCAACAACAATCATTCATCTACTCACTCAATA 899

QY      1505  GCAACTCTGGGAGAGCCTGGAGCATTCGGACTTGGCCCTATGGGAGGGGAGCGCTGGAG 1564

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Db 900 GCAACACTGGGAGAGCCCTGGAGCAGCCGAGCTTGCCCTGTGGGAGAGGGGACACTGGAG 959
QY 1565 GAGTGGCTGCATCTATCTGATATATACAGACCCCTGT 1599
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RESULT 4
US-11-266-748A-346502/c
; Sequence 346502, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 346502
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-346502

Query Match 55.2%; Score 883; DB 8; Length 1000;
Best Local Similarity 94.3%; Pred. No. 8.3e-234;
Matches 938; Conservative 0; Mismatches 55; Indels 2; Gaps 2;

QY 606 ACACAGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACC 665
Db 1000 ACACAGAAATTGGGCCCGTGGGTATGACTGAGAACTGCGATATGAAAGATTTCTGACC 941

QY 666 TGTCATCGGGGACCAACCATATGACACAGGAACTTGCTCAAGAACCACTGATTGG 725
Db 940 TGTCATCGGGGACCACTTTGAAGAAGCAGGAAACTTGATGAAGAACCACTGATTGG 881

QY 726 ACCACATCGAATACCGAGATGTGCGAGTGGGCGAGTGTGTCAGGAGACGCTGTGCTC 785
Db 880 GCCACATCTAATACCGAGAGCTGGAGTGGGCGAGTGTGTCAGGAGATGCTGTGCTC 821

QY 786 ATAGATGTAGGACTCACATCAACCCCTGGTGGGGAACAAAGGCTGCAGCACTGTGGGGCT 845
Db 820 ATAGATGTAGGACTCACATCAACCCCTGGTGGGACCTAAAGCTGCAGCGCTGTGGGGCT 761

QY 846 CAAAAATCCAGAGACCAACATCCATCAGCCCTCTGGGTGCTTGTGGGCTCTAT 905
Db 760 CAAAAATCCAGAGACCAACATCCATCAGCCCTCTGGGTGCTTGTGGGCTCTAT 701

QY 906 ACCCACTTCTGCTCTCGGACCTGTGCAATAGTCCAGCAGCAGCAGCGCTTCTGCTGAAC 965
Db 700 ACCCACTTCTGCTCTCGGACCTGTGCAATAGTCCAGCAGCAGCAGCGCTTCTGCTGAAC 641

QY 966 TCCCTCCCTCCTCAAGCTGCCCCCTGTGCCAGGAGACCGGAGTGTCTTACCTGTGTGCGAG 1025
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Db 640 TCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGAGTGTCTTACCTGTGTGCGAG 581
QY 1026 CCCCTTGGAACTCTTTCAAGTGGCTCCCCCGCAATGACCTGCCCGGAGGGGCGCACTCAT 1085
Db 580 CCCCTTGGAACTCTTTCAAGTGGCTCCCCCGCAATGACCTGCCCGGAGGGGCGCACTCAT 521
QY 1086 TGTATGATGGGTACATTCATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCAATTCAG 1145
Db 520 TGTATGATGGGTACATTCATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCAATTCAG 461
QY 1146 GCGTGGTGGCCCAACCTTCCAGCTTCTTTGTAACCAACACACAGCAAAATCGGGATCTTC 1205
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QY 1326 GGAGTGGTTGGCTTCTGCTGCTAACTCTATATACCCCAACAGATTCCTCAGCGCTGCGAC 1385
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QY 1386 ACCCAGCTCAACCTCCCTCTGACCTCATAACCTAATGGCTTGGACACAGATTCCTTT - 1444
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QY 1445 CCCATTCTGTCCATGAATCATCTTCCCAACACACAAATCATTCATCTTCACTACCTAAC 1504
Db 161 CCCATCTCTGCCATGAATCATCTTCCCAACACACAAATCATTCATCTTCACTACCTAAC 102
QY 1505 GCACACTGGGAGAGCCCTGGAGCATCCGAGCTTGGGCTTGGGAGGGGAGCGCTGGAG 1564
Db 101 GCAACACTGGGAGAGCCCTGGAGCAGCGGACTTGGCCCTGTGGGAGGGGAGCACTGGAG 42
QY 1565 GAGTGGCTGCATGTATCTGATATACAGACCCCTGT 1599
Db 41 GAGTGGCTGCATGTGTCTGATATATAAGACCCCTGT 7

RESULT 5
US-11-266-748A-215833/c
; Sequence 215833, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
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NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 215833  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (48)..(48)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-215833

Query Match 54.6%; Score 874.4; DB 8; Length 1000;  
Best Local Similarity 98.9%; Pred. No. 2e-231;  
Matches 889; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 650 GAAAGATTTTCTGACCTGTCTATCGGGGACCAACCATATGACACACGGAACCTTGGCTCA 709  
Db |  
Qy 898 GAAAGATTTTCTGACCTGTCTATC-GGGGACCAACCATATGACACACGACACTTGTCTCA 840  
Db |  
Qy 710 AGAACCCACTGATTGGACCAATCGAATACCGAGATGCGAGGTGGGAGGTGTCTCA 769  
Db |  
Qy 839 AGAACCCACTGATTGGACCAATCGAATACCGAGATGCGAGGTGGGAGGTGTCTCA 780  
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Qy 770 GGAGACGCTGCTCTATAGATGATGAGACTCACATCAACCTGTGGTGGGACAAAAGGCTG 829  
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Qy 779 GGAGACGCTGCTCTCTAGATGTAGAACTCACATCAACCTGTGGTGGGACAAAAGGCTG 720  
Qy 830 CAGCACTGTTGGGCTCAAAATTCAGAGAACCAACCATCACTCAGCCCCCTCTCTGGGCT 889  
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Qy 719 CAGCACTGTTGGGCTCAAAATTCAGAGAACCAACCATCACTCAGCCCCCTCTCTGGGCT 660  
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Db |  
Qy 659 GCTTGTGGGCTCTTATACCACTTCTCTCTCGAGCTGTGCAATGTCAGACGAG 600  
Qy 950 CAGGCTTCTGTGAACCTCCCTCTCTCAAGCTGCCCTGTCCAGAGACCGGAGTG 1009  
Db |  
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Qy 539 TCCTACTGTGTGAGCGCCCTTGAACCTGTTCAGTGGCTTCCCTCCGAATGACTCGCC 480  
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Qy 479 CAGGGGCGCACTATTGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
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Qy 179 TTCAACCGCTGTGACACCACTCAACCTTCCCTCTGACCTCATAACCTTAATGGCCTTG 120  
Qy 1430 GACACGAGATTTCTTCCATTTCTGTCCATGATCATCTTCCCAACACATGATTCATA 1489  
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RESULT 6

US-11-266-748A-237848  
; Sequence 237848, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 5815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
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; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 237848  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (953)..(953)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-237848

Query Match 54.6%; Score 874.4; DB 8; Length 1000;  
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Matches 889; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 650 GAAAGATTTTCTGACCTGTCTATCGGGGACCAACCATATGACACACGGAACCTTGGCTCA 709  
Db |  
Qy 103 GAAAGATTTTCTGACCTGTCTATC-GGGGACCAACCATATGACACACGACACTTGTCTCA 161  
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Qy 710 AGAACCCACTGATTGGACCAATCGAATACCGAGATGCGAGGTGGGAGGTGTCTCA 769  
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Qy 162 AGAACCCACTGATTGGACCAATCGAATACCGAGATGCGAGGTGGGAGGTGTCTCA 221  
Qy 770 GAGAGCCTGCTGCTCTATAGATGATGAGACTCAATCAACCTGTGGTGGGACAAAAGGCTG 829  
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Qy 222 GAGAGCCTGCTGCTCTCTAGATGTAGAACTCACATCAACCTGTGGTGGGACAAAAGGCTG 281  
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Qy 282 CAGCACTGTTGGGCTCAAAATTCAGAGAACCAACCATCACTCAGCCCCCTCTCTGGGCT 341  
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Query Match 39.2%; Score 627.4; DB 8; Length 654;  
Best Local Similarity 99.8%; Pred. No. 2,9e-163;  
Matches 628; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 941 CAGCAGCAGCAGCGTTCTGCTGAACTCTCCCTCTCAAGCTGCCCTGTCCAGGAGA 1000  
DB 26 CAGCAGCAGCAGCGTTCTGCTGAACTCTCCCTCTCAAGCTGCCCTGTCCAGGAGA 85  
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QY 1181 CCACACCAGACAAATCGGGATCTTCTCTCGCGTGAAGCGTGTGAGCGCTCTCTGC 1240  
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QY 1301 GGCACGTGGCCCCAGCGCTGTGTGGGAGTGGTTTGGCTTCTCTGCTAACTCTATTACCC 1360  
DB 386 GGCACGTGGCCCCAGCGCTGTGTGGGAGTGGTTTGGCTTCTCTGCTAACTCTATTACCC 445  
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RESULT 8

US-11-266-748A-17659  
; Sequence 17659, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266, 748A  
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; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03

RESULT 7

US-11-266-748A-2984  
; Sequence 2984, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
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; PRIOR APPLICATION NUMBER: US 60/662, 276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700, 293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2984  
; LENGTH: 654  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-2984



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; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17659
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-17659

Query Match      37.4%; Score 597.8; DB 8; Length 749;
Best Local Similarity 99.5%; Pred. No. 4.7e-155;
Matches 610; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 987 CTTGTCCTCCAGGAGACCGGCGAGTGTCTTACCTGTGTGAGGCCCTTTGGAACCTGTTCAAGT 1046
Db      |||||
QY 137 CTTGTCCTCCAGGAGACCGGCGAGTGTCTTACCTGTGTGAGGCCCTTTGGAACCTGTTCAAGT 196
Db      |||||
QY 1047 GGCTCCCTCCGATGACTGCTCCAGGGGGCGCCACTCATTTGTTATGATGGGTACATTCAT 1106
Db      |||||
QY 197 GGCTCCCTCCGATGACTGCTCCAGGGGGCGCCACTCATTTGTTATGATGGGTACATTCAT 256
Db      |||||
QY 1107 CTCTCAGGAGGTGGGCTGTCACCAAAATGAGCAATTCAGGGCTGCGTGGGCCACCTTCC 1166
Db      |||||
QY 257 CTCTCAGGAGGTGGGCTGTCACCAAAATGAGCAATTCAGGGCTGCGTGGGCCACCTTCC 316
Db      |||||
QY 1167 AGCTTCTTGTGTAACACACACAGACAAATCGGATCTTCTCTGCGCTGAGAACGCTGAT 1226
Db      |||||
QY 317 AGCTTCTTGTGTAACACACACAGACAAATCGGATCTTCTCTGCGCTGAGAACGCTGAT 376
Db      |||||
QY 1227 GTGAGAGCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTTGGAGTCTCTCACT 1286
Db      |||||
QY 377 GTGAGAGCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTTGGAGTCTCTCACT 436
Db      |||||
QY 1287 TGGGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1346
Db      |||||
QY 437 TGGGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 496
Db      |||||
QY 1347 TAACCTATTATACCCCAACGATTTCTTACCGCTGTGACCCACCACTCAACCTCCCTCT 1406
Db      |||||
QY 497 TAACCTATTATACCCCAACGATTTCTTACCGCTGTGACCCACCACTCAACCTCCCTCT 556
Db      |||||
QY 1407 GACCTATAACCTAAATGGCTTGGACACCAAGATTTCTTCCATTTCTTCATGAATCATC 1466
Db      |||||
QY 557 GACCTATAACCTAAATGGCTTGGACACCAAGATTTCTTCCATTTCTTCATGAATCATC 616
Db      |||||
QY 1467 TTCCCAACACATCAATTCATATCTACTACCTAACGACCACTGGGGAGGCTTGA 1526
Db      |||||
QY 617 TTCCCAACACATCAATTCATATCTACTACCTAACGACCACTGGGGAGGCTTGA 676
Db      |||||
QY 1527 GCATCCCGAATTGGCCCTAT--GGGAGAGGAGCGCTGGAGGAGTGGCTGCGATGATCTGAT 1585
Db      |||||
QY 677 GCATCCCGAATTGGCTATGGGAGAGGAGCGCTGGAGGAGTGGCTGCGATGATCTGAT 736
Db      |||||
QY 1586 AATACAGACCTG 1598
Db      |||||
QY 737 AATACAGACCTG 749
Db      |||||
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RESULT 9  
US-11-266-748A-54407  
; Sequence 54407, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same

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; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54407
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-54407
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Query Match      32.2%; Score 516; DB 8; Length 549;
Best Local Similarity 97.8%; Pred. No. 1.6e-132;
Matches 534; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

QY 1026 CCCCTTGGAACTGTTCAAGTGGCTCCCGG--AATGACCTGCCCCAGGGGCGCCACTC 1083
Db      |||||
QY 1084 ATTGTTATGATGGGTACATTCATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCATTC 1143
Db      |||||
QY 64 ATTGTTATGATGGGTACATTCATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCATTC 123
QY 1144 AGGCTCGTGGGCCCAACCTTCCAGCTTCTTGTGAACCAACAGAGAAATCGGGATCT 1203
Db      |||||
QY 124 AGGCTCGTGGGCCCAACCTTCCAGCTTCTTGTGAACCAACAGAGAAATCGGGATCT 183
QY 1204 TCTCTGCGCTGAGAGCGTGTGAGCTCTCTGCTCTCTCAGCATGAGGAGGTGGG 1263
Db      |||||
QY 184 TCTCTGCGCTGAGAGCGTGTGAGCTCTCTGCTCTCTCAGCATGAGGAGGTGGG 243
QY 1264 CTGAGGCGCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCCAGCGCTGTGGT 1323
Db      |||||
QY 244 CTGAGGCGCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCCAGCGCTGTGGT 303
QY 1324 GGGGAGTGGTTGGCTTCTCTGCTTACTTATACCCCGAGGATCTTACCGCTGTGTA 1383
Db      |||||
QY 304 GGGGAGTGGTTGGCTTCTCTGCTTACTTATACCCCGAGGATCTTACCGGATGTA 363
QY 1384 CCACCCACACTCAACCTTCCCTCTGACCTATACTAATGSCCTTGGACACCAAGATCTT 1443
Db      |||||
QY 364 CCACCCACACTCAACCTTCCCTCTGACCTATACTAATGSCCTTGGACACCAAGATCTT 423
QY 1444 TCCCATTTCTGTCATGAATCATCTTCCCAACACACAAATCATTTACTTACTTCACTTAAC 1503
Db      |||||
QY 424 ACCCATTTCTGTCATGAATCATCTTCCCAACACACAAATCATTTACTTACTTCACTTAAC 483
QY 1504 AGCAACACTGGGAGAGCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGGAGCTGGA 1563
Db      |||||
QY 484 AGCAACACTGGGAGAGCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGGAGCTGGA 543
QY 1564 GGAGTG 1569
Db      |||||
QY 544 GGAGTG 549
Db      |||||
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RESULT 10



QY 1139 CATTGAGGCTGCGTGGCCCAACCTTCAGCTTCTTGTTGAACACACACACGACAAATCGG 1198  
Db 708 GGTCAAGGCTGTACAGCCATGATGGCTGAGGCTGATGCTGGAATCTTAGCAGTAGG 767  
QY 1199 GATCTTCTCTCGCGGTGA 1216  
Db 768 ACCCATGTTGTGAGGGA 785

## RESULT 12

US-11-266-748A-451387/c  
; Sequence 451387, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 5815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: Patencin version 3.3  
; SEQ ID NO 451387  
; LENGTH: 1037  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-451387

Query Match 4.6%; Score 74; DB 8; Length 1037;  
Best Local Similarity 51.0%; Pred. No. 3.1e-10;  
Matches 254; Conservative 0; Mismatches 235; Indels 9; Gaps 3;  
QY 719 TGATTGACACATCGAATACCGAGATGTGGAGGTGGGAGGTGTGTCAGGAGCGCT 778  
Db 741 TAACTGGACACACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 682  
QY 779 GCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGACAAAGGCTGCAGCACTGT 838  
Db 681 ACTAATAATTAAGACAGGACTGAGACAGCCATTTTGGCCACGAGGGCTGCATCCCGA 622  
QY 839 TGGGGCTCAAAATTTCCAGAAAGACCAATCCATCCAGCCCTCTCTGGGGTGTCTTGGC 898  
Db 621 AGGGG---AGGAGGCCATAACAATTGTCAGCACTCTTCACTCCCGGCTGATCGTGAC 565  
QY 899 CTCCTATACCACTTCTGCTCTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTCT 958  
Db 564 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCCTGTCTCAGTT 505  
QY 959 GCTGAACTCCCTCCCTCAAGCTGCCCTGTCCAGGAGACGGGAGGTGCTTACCTG 1018  
Db 504 TTGGAGTTCAGTGAGACCAACAGCTTCCACTGTGTCAACACCTCCCTATGTCCAACTG 445  
QY 1019 TGTGCACCCCTTGGAACTGTTCAGTGGCTCCCGCCGAATGACCTGCCCGCAGGGCGC 1078  
Db 444 TGT---GGCTTTGGGACCTGTTTACGTG---CTCCCTTCTTCTTCCCTGTCCCAATGTATC 391

QY 1079 CACTCATTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGCCACCAAAATGAG 1138  
Db 390 AACTCGATGTCTACAGGAAACCTTGAGATCACTGGAGGTGGCATGATGCTCTGTGGA 331  
QY 1139 CATTGAGGCTGCGTGGCCCAACCTTCAGCTTCTTGTTGAACACACACGACAAATCGG 1198  
Db 330 GGTCAAGGCTGTACAGCCATGATGGCTGAGGCTGATGCTGGAATCTTAGCAGTAGG 271  
QY 1199 GATCTTCTCTCGCGGTGA 1216  
Db 270 ACCCATGTTGTGAGGGA 253

## RESULT 13

US-11-266-748A-291309  
; Sequence 291309, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 5815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: Patencin version 3.3  
; SEQ ID NO 291309  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-291309

Query Match 4.6%; Score 73.2; DB 8; Length 1000;  
Best Local Similarity 48.0%; Pred. No. 5e-10;  
Matches 306; Conservative 0; Mismatches 323; Indels 9; Gaps 3;  
QY 719 TGATTGACACATCGAATACCGAGATGTGGAGGTGGGAGGTGTGTCAGGAGCGCT 778  
Db 141 TAACTGGACACACAGAGGAAGTGGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCAT 200  
QY 779 GCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGACAAAGGCTGCAGCACTGT 838  
Db 201 ACTAATAATTAAGACAGGACTGAGACAGCCATTTTGGCCACGAGGGCTGCATCCCGA 260  
QY 839 TGGGGCTCAAAATTTCCAGAAAGACCAATCCATCCAGCCCTCTCTGGGGTGTCTTGGC 898  
Db 261 AGGGG---AGGAGGCCATAACAATTGTCAGCACTCTTCACTCCCGGCTGATCGTGAC 317  
QY 899 CTCCTATACCACTTCTGCTCTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTCT 958  
Db 318 CTCCTACAGTAACTACTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCCTGTCTCAGTT 377  
QY 959 GCTGAACTCCCTCCCTCAAGCTGCCCTGTCCAGGAGACGGGAGGTGCTTACCTG 1018

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Db 378 TTGGGAGTTCACTGAGACACACAGCTTCCACTGTGTCAACAACCCCTCCATTGTGTCCAACCTG 437
QY 1019 TGTGACGCCCTTGGAACTGTTCAAGTGTGCTCCCTCCCGAATGACCTGCCCCAGGGGGCGC 1078
Db 438 TGT---GGCTTTGGGAGCTGTTTCAGTGTCTCTTCTC---TTCCCTATCCCAATGGTAC 491
QY 1079 CACTCATTTGATGAGGTGACATTCATCTCTCAGAGGTGGGCTGTCCACCAAAATGAG 1138
Db 492 AACTCGATGCTATCAAGGAAACTTTCAGATCACTGAGGTGGCATTTGAGTGTCTGTGGA 551
QY 1139 CATTCAGGGCTGGTGGCCCAACCTTCCAGCTTCTTGTGTAACCAACACAGACAAATCG 1198
Db 552 GGTCAAGGCTGTACAGCCATGATTTGGCTGCGAGCTGATGTCTGGAATCTTAGCAGTAGG 611
QY 1199 GATCTTCTCTGGCGGTGAGAAGCGTGTGTGACGCTCTCTGCGCTCTCAGCATGAGGGAG 1258
Db 612 ACCATGTTTGTGAGGAAGCGTGGCCACATCAGCTGTCTCACTCAACCTTGGAAAGACTGA 671
QY 1259 TGGGGCTGAGGGCTGGAGTCTCTCACTTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCT 1318
Db 672 AAATGGGGCCACCTGTCTCCCATTCCTGTGTTGGGGGTTACAGCTACTGCTGCCATTGCT 731
QY 1319 GTGGTGGGAGTGGTTGGCTTCCCTCTGCTTAACCTATT 1356
Db 732 GCTGCCATCATTTATTCACTTTTCTTAAGAAGGCACCTT 769

RESULT 14
US-11-266-748A-342738/c
; Sequence 342738, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 342738
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-342738

Query Match 4.6%; Score 73.2; DB 8; Length 1000;
Best Local Similarity 48.0%; Pred. No. 5e-10;
Matches 306; Conservative 0; Mismatches 323; Indels 9; Gaps 3;

QY 719 TGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTGTCAGGAGACGCT 778
Db 860 TAATCGACACACAGAGGAAGTGGAGCTTTGTGACAAAGGGGCACTTTGCCAGGAACCAT 801
QY 779 GCTGCTCATAGATGTAGGACTCATCATCAACCTTGGTGGGGACAAAGGGCTGCAGCACTGT 838
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Db 800 ACTATAATATAAGCAGGACTGAGACAGCCATTTTGGCCACGAAGGGTGCATCCGGA 741
QY 839 TGGGGCTCAAAATTTCCAGAAGACCAACCATCCACTCAGCCCCCTCTCTGGGGTGTCTGTGGC 898
Db 740 AGGG---AGGAGGCATTAACATTTGTCCAGACACTTTCACCTCCGGGCTGATCGTGAC 684
QY 899 CTCTCATACCCACTTCTGTCTCTCGGA CTTGTGCAATAGTGGCAGCAGCAGCGTCTT 958
Db 683 CTCTACAGTAACACTGTGTGAGGATTCCTTCTGTAATGACAAAGACAGCCCTGTCTCAGTT 624
QY 959 GCTGAATCCCTCCCTCCCTCAAGCTGCCCCCTGTCCAGGAGAGCGGCGAGTGTCTTACCTG 1018
Db 623 TTGGGAGTTTCAGTGAAGACCAACAGCTTCCACTGTGTCAACAACCTCCATTTGCCAACCTG 564
QY 1019 TGTGACGCCCTTGGAACTGTTCAAGTGGCTCCCCCGAAATGACCTGCCCCAGGGGGCGC 1078
Db 563 TGT---GGCTTTGGGACCTGTTTCAGTGTCTCTTCTC---TTCCCTATCCCAATGGTAC 510
QY 1079 CACTCATTTGATGAGGTGACATTCATCTCTCAGAGGTGGGCTGTCCACCAAAATGAG 1138
Db 509 AACTCGATGCTATCAAGGAAACTTTCAGATCACTGAGGTGGCATTTGAGTGTCTGTGGA 450
QY 1139 CATTCAGGGCTGGTGGGCCCAACCTTCCAGCTTCTTGTGTAACCAACACAGACAAATCG 1198
Db 449 GGTCAAGGCTGTACAGCCATGATTTGGCTGCGAGGCTGATGTCTGGAATCTTAGCAGTAGG 390
QY 1199 GATCTTCTCTGGCGGTGAGAAGCGTGTGTGACGCTCTCTGCGCTCTCAGCATGAGGGAGG 1258
Db 389 ACCATGTTTGTGAGGAAGCGTGGCCACATCAGCTGTCTCACTCAACCTTGGAAAGACTGA 330
QY 1259 TGGGGCTGAGGGCTGGAGTCTCTCACTTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCT 1318
Db 329 AAATGGGGCCACCTGTCTTCCCATTCCTGTGTTGGGGGTTACAGCTACTGCTGCCATTGCT 270
QY 1319 GTGGTGGGAGTGGTTGGCTTCCCTCTGCTTAACCTATT 1356
Db 269 GCTGCCATCATTTATTCACTTTTCTTAAGAAGGCACCTT 232

RESULT 15
US-11-266-748A-368007/c
; Sequence 368007, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368007
; LENGTH: 1092
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-368007

Query Match      4.5%; Score 72.4; DB 8; Length 1092;
Best Local Similarity 50.8%; Pred. No. 8.7e-10;
Matches 253; Conservative 0; Mismatches 236; Indels 9; Gaps 3;

Qy 719 TGATGGACACATCGAGATGTCGAGGTGGGGCAGGTGTCTCAGGAGACGCT 778
Db      |||||
Qy 762 TAACTGGACACAGAGAGTGGAGACTTGTGACAAAGGGGCACTTCCAGGAACCAT 703
Db      |||||
Qy 779 GCTGCTCATAGATAGGACTCACATCAACCTGGTGGGGACAAAAGGCTGCAGCACTGT 838
Db      |||||
Qy 702 ACTAATAATTAAAGCAGGACTGAGACAGCCATTTGGCCACGAAGGCTGCATCCCGGA 643
Db      |||||
Qy 839 TGGGCTCAAAATTCAGAGAGACCAAGATCCACTCAGCCCTCTCTGGGGTGTCTTGTGGC 898
Db      |||||
Qy 642 AGGGG---AGGAGGCCATAACAATTGTCCAGCACTTTCACCTCCGGCCTGATCGTGAC 586
Db      |||||
Qy 899 CTCCTATACCACCTTCGTCTCTCGGACCTGTGCAATAGTGCCAGCAGCAGCGTTCT 958
Db      |||||
Qy 585 CTCCTACAGTAACACTACTGTGAGGATTCCTCTGTAATGACAAAGACAGCCTGTCTCAGTT 526
Db      |||||
Qy 959 GCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTCTCTAGCTG 1018
Db      |||||
Qy 525 TTGGAGTTCAGTGAGACCAAGCTTCCACTGTGTCAACACCCTCCATTGTCCAACCTG 466
Db      |||||
Qy 1019 TGTGACGCCCTTGGAAACCTGTTCAGTGGCTCCCGCCGAATGACCTGCCCGCAGGGGGCC 1078
Db      |||||
Qy 465 TGT---GGCTTTGGGGACCTGTTTCAGTG---CTCCTTCTCTCCCTGTCCCAATGGTAC 412
Db      |||||
Qy 1079 CACTCATTTATCATGGGTACATTCATCTCTCAGGAGTGGGCTGCCACCAAAATGAG 1138
Db      |||||
Qy 411 AACTCGATGCTATCAAGGAAACCTTGAGATCCTGGAGGTGGCATTGAGTGTCTGTGGA 352
Db      |||||
Qy 1139 CATTCAGGGCTGGTGGCCCAACCTTCCAGCTTCTTGTGTGAACCAACACAGACAAATCGG 1198
Db      |||||
Qy 351 GGTCAAAGGCTGTACACCCATGATTGGCTGCAGGCTCATGTCTGGAATCTTAGCAGTAGG 292
Db      |||||
Qy 1199 GATCTTCTCTGGCGTGA 1216
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Qy 291 ACCCATGGTTGTGAGGA 274
Db      |||||
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GenCore version 5.1.9  
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9282.444 Million cell updates/sec

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Perfect score: 1600  
Sequence: 1 aaagcagaagagattacc.....ctgataatacacagacctgtc 1600

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
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- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1600	100.0	1600	9	US-10-727-619-1
2	1599.6	100.0	1630	9	US-10-723-860-3881
3	1598.4	99.9	1692	9	US-10-723-860-7799
4	1579.4	98.7	1587	3	US-09-989-722-354
5	1579.4	98.7	1587	3	US-09-989-723-354
6	1579.4	98.7	1587	3	US-09-989-279-354
7	1579.4	98.7	1587	3	US-09-989-727-354
8	1579.4	98.7	1587	3	US-09-989-731-354
9	1579.4	98.7	1587	3	US-09-989-732-354
10	1579.4	98.7	1587	3	US-09-991-073-354
11	1579.4	98.7	1587	3	US-09-990-442-354
12	1579.4	98.7	1587	3	US-09-991-163-354
13	1579.4	98.7	1587	3	US-09-993-604-354
14	1579.4	98.7	1587	3	US-09-990-456-354
15	1579.4	98.7	1587	3	US-09-989-721-354
16	1579.4	98.7	1587	3	US-09-992-598-354
17	1579.4	98.7	1587	3	US-09-989-293A-354

18	1579.4	98.7	1587	3	US-09-989-735-354	Sequence 354, App
19	1579.4	98.7	1587	3	US-09-990-444-354	Sequence 354, App
20	1579.4	98.7	1587	3	US-09-991-181-354	Sequence 354, App
21	1579.4	98.7	1587	3	US-09-989-730-354	Sequence 354, App
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23	1579.4	98.7	1587	3	US-09-993-687-354	Sequence 354, App
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44	1579.4	98.7	1587	3	US-09-997-601-354	Sequence 354, App
45	1579.4	98.7	1587	3	US-09-990-443-354	Sequence 354, App

ALIGNMENTS

RESULT 1  
US-10-727-619-1  
; Sequence 1, Application US/10727619  
; Publication No. US20040259110A1  
; GENERAL INFORMATION:

; APPLICANT: PAHL, HEIKE  
; TITLE OF INVENTION: PRV-1 AND THE USE THEREOF  
; FILE REFERENCE: LEDER-1  
; CURRENT APPLICATION NUMBER: US/10/727,619  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/830,189  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/EP99/07238  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 198 49 044.5  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1600  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-727-619-1

Query Match	100.0%;	Score 1600;	DB 9;	Length 1600;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1600;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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RESULT 2

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US-10-723-860-3881
; Sequence 3881, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3881
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-723-860-3881
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-10-723-860-7799  
; Sequence 7799, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7799  
; LENGTH: 1692  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-7799

Query Match 99.9%; Score 1598.4; DB 9; Length 1692;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1599; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1201 TCTTCTCTCGGTGAGAGCGGTGATGTGAGCGCTCTCTGAGCTTCTTGTGAACACAGAGGTG 1260  
QY 1261 GGGCTAGGGCCCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCGCAGCGCTCT 1320  
DB 1261 GGGCTAGGGCCCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCGCAGCGCTCT 1320  
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DB 1381 TGACCAACCACTCAACCTCTCTGACCTCTATAAATGAGGTGGGCTGGGAGGAGGAT 1440  
QY 1441 CTTTCCCATTTCTGTCATGATCACTTCTCCCAACACATCAATCTATCTACTCACT 1500  
DB 1441 CTTTCCCATTTCTGTCATGATCACTTCTCCCAACACATCAATCTATCTACTCACT 1500  
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RESULT 4  
US-09-989-722-354  
; Sequence 354, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC63  
; CURRENT APPLICATION NUMBER: US/09/989,722  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	20	CAGCCACAGACGGGTGATGAGCGGTATTACTGCTGGCCCTCTCTGGGGTTTCATCCTCCC	79
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Qy	80	ACTGCCAGGAGTGACGGCGTCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT	139
Db	61	ACTGCCAGGAGTGACGGCGTCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT	120

140 GTCCGACCTGCCCGCAATGGACCCCTAAGAACACCAAGTCGACAGCGGCTTGGGGTG 199  
121 GTCCGACCTACCCCGCANTGACCCCTAAGAACACCAAGTCGACAGCGGCTTGGGGTG 180  
200 CCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCTGCTCTCCAAAGG 259  
181 CCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCTGCTCTCCAAAGG 240  
260 CTGCGAGGAGGCCAAGGACCAAGAGCCCGCGTCACTGAGCACCGGATGGGCCCGGCT 319  
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601 GCCCGTGGTATGACTGAGAACTGCAATAGGAAGATTTCTGACCTGTCTATCGGGGAC 660  
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## RESULT 5

US-09-989-723-354  
; Sequence 354, Application US/09989723  
; Patent No. US2002007292A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC62  
; CURRENT APPLICATION NUMBER: US/09/989, 723  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
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4	PRIOR APPLICATION NUMBER: 60/083322	5	PRIOR FILING DATE: 1998-06-17
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6	PRIOR APPLICATION NUMBER: 60/084600	7	PRIOR FILING DATE: 1998-06-17
7	PRIOR FILING DATE: 1998-05-07	8	PRIOR APPLICATION NUMBER: 60/089653
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20	PRIOR APPLICATION NUMBER: 60/088025	21	PRIOR FILING DATE: 1998-06-19
21	PRIOR FILING DATE: 1998-06-04	22	PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 80 ACTGCCAGGAGTGCAGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAAGT 139  
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QY 140 GTCCGACCTGCCCGGCAATGGACCCCTAAGAACACCACTGCGACAGCGGCTTGGGGTG 199  
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QY 200 CAGGACAGTTGATGCTGATAGAGCGGACCCCAAGTAGAGCTGCTGCTCCCAAGG 259  
DB 181 CCAGGACAGTTGATGCTGATAGAGCGGACCCCAAGTAGAGCTGCTGCTCCCAAGG 240

QY 260 CTGACGGAGGCCAAGGACCCAGGACCCGCGCTCACTGAGCAGCGATGGGCCCGGCGCT 319  
DB 241 CTGACGGAGGCCAAGGACCCAGGACCCGCGCTCACTGAGCAGCGATGGGCCCGGCGCT 300

QY 320 CTCCTCTGATCTCTACACCTTCTGTCGCCCGCAGGAGGACTTCTGCAACACCTCGTTAA 379  
DB 301 CTCCTCTGATCTCTACACCTTCTGTCGCCCGCAGGAGGACTTCTGCAACACCTCGTTAA 360

QY 380 CTCCTCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGAGGTGCCAGT 439  
DB 361 CTCCTCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGAGGTGCCAGT 420

QY 440 CTCCTTGTCTATGAAAGGCTGCTGAGAGGGGACAAAGAGAGATCTGCCCAAGGGAC 499  
DB 421 CTCCTTGTCTATGAAAGGCTGCTGAGAGGGGACAAAGAGAGATCTGCCCAAGGGAC 480

QY 500 CACACACTGTTATGATGGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCCAATCTGAG 559  
DB 481 CACACACTGTTATGATGGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCCAATCTGAG 540

QY 560 AGTCCAGGATGATGCCCCAGCGAGTTGCAACCTGCTCAATGGGACACAGAAATGG 619  
DB 541 AGTCCAGGATGATGCCCCAGCGAGTTGCAACCTGCTCAATGGGACACAGAAATGG 600

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QY 680 CACCATTTATGACACACGAAACTTGGCTCAAGAACCCACTGATTTGGACCATCGAATAC 739  
DB 661 CACCATTTATGACACACGAAACTTGGCTCAAGAACCCACTGATTTGGACCATCGAATAC 720

QY 740 CGAGATGTGCGAGGTGGGCGAGTGTGTACAGGAGCGCTGCTCATAGATGAGACT 799  
DB 721 CGAGATGTGCGAGGTGGGCGAGTGTGTACAGGAGCGCTGCTCATAGATGAGACT 780

QY 800 CACATCAACCTCTGTGGGGACAAAGGCTCAGCAGCTTTGGGCTCAAAATTTCCAGAA 859  
DB 781 CACATCAACCTCTGTGGGGACAAAGGCTCAGCAGCTTTGGGCTCAAAATTTCCAGAA 840

QY 860 GACCACCATCACTCAGCGCCCTCTCTGGGGGTGCTTGTGGGCTCTCTATACCCACTTCTGCTC 919

DB 841 GACCACCATCCACTCAGCCCCCTCTGGGGTGTCTTGTGGCTCTCTATACCACTTCTGCTC 900

QY 920 CTCGGACCTGTGCAATAGTCCAGACAGCAGCGCTTCTGCTGAACTCCCTCCTCTCTCA 979

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DB 1321 TTCTCTGCTAACTCTATTACCCCAACCAATCTTCAACCGCTGCTGACCACTCAAC 1380

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DB 1381 TCCTCTGACCTCATTAACCTAATGGCTTGGGACACAGATTTCTTCCACTTCTGTCATG 1440

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DB 1501 GCCTGGAGCATCGGACTTGGCTTGGGAGGGGACGCTGGAGGAGTGGCTGCAATGTA 1560

QY 1580 TCTGATAATACAGACCTGTC 1600

DB 1561 TCTGATAATACAGACCTGTC 1581

RESULT 6  
US-09-989-279-354  
; Sequence 354, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989,279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
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PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
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PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557







Db 1561 TCTGATAATACAGACCCCTGTC 1581

RESULT 7

US-09-989-727-354

Sequence 354, Application US/09989727

Patent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCES: P2730P1C65

CURRENT APPLICATION NUMBER: US/09/989,727

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

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/	PRIOR APPLICATION NUMBER: 60/091982	
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/	PRIOR FILING DATE: 1998-07-09	
Query Match 98.7%; Score 1579.4; DB 3; Length 1587;		
Best Local Similarity 99.9%; Pred. No. 0;		
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
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Db	61	ACTGCCAGGAGTGCAGGCGTGTCTGCCAGTTTGGGACAGTTTTCAGCATGTGTGGAGGT 120
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QY	740	CGAGATGTGCGAGGTGGGCGAGTGTCTCAGGAGAGCTGCTCTCATAGATGTAGGACT 799
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QY	800	CACATCAACCTCTGTGGGACAAAAGGCTGCAGACCTGTGGGGCTCAAAATTTCCAGAA 859
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QY	920	CTCGGACCTGTGCAATAGTGCAGCAGCAGCGCTTCTGCTGAACCTCCCTCTCTCA 979
Db	901	CTCGGACCTGTGCAATAGTGCAGCAGCAGCGCTTCTGCTGAACCTCCCTCTCTCA 960
QY	980	AGCTGCCCTCTGTCCAGGAGACCGGAGTGTCTTACTGTGTGAGCCCTTGGAACCTG 1039
Db	961	AGCTGCCCTCTGTCCAGGAGACCGGAGTGTCTTACTGTGTGAGCCCTTGGAACCTG 1020
QY	1040	TTCAAGTGGCTCCCCCGAATGACCTGCCCGGAGGAGGCTGCTGTTATGATGGGTA 1099
Db	1021	TTCAAGTGGCTCCCCCGAATGACCTGCCCGGAGGAGGCTGCTGTTATGATGGGTA 1080
QY	1100	CATTATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159
Db	1081	CATTATCTCTCAGGAGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140
QY	1160	ACCTTCAGGCTTCTTGTGAAACCAACAGCAAAATCGGGATCTTCTCTGGCGGTGAGAA 1219
Db	1141	ACCTTCAGGCTTCTTGTGAAACCAACAGCAAAATCGGGATCTTCTCTGGCGGTGAGAA 1200
QY	1220	GGTGTGATGTGACCTCTGCTCTCAGCATGAGGAGGTGGGCTCAGGGCTTGGAGTC 1279

Db	1201	GCGTGATGTGCAGCCTCCTCTCAGCATGAGGGAGTGGGGCTGAGGGCCTTGGAGTC	1260
Qy	1280	TCTCACTTGGGGGTGGGGCTGGCACTGGGCCCAAGCAGCGTGTGTGGGGAGTGGTTTCCCC	1339
Db	1261	TCTCACTTGGGGGTGGGGCTGGCACTGGGCCCAAGCAGCGTGTGTGGGGAGTGGTTTCCCC	1320
Qy	1340	TTCCTGTAACTCTATTACCCCAACGATTTCTTCAACCGCTGCTGACCAACCACCACTCAACC	1399
Db	1321	TTCTGTGTAACCTTATTACGCCACGATTTCTTCAACCGCTGCTGACCAACCACCACTCAACC	1380
Qy	1400	TCCCTCTGACCTCATATAACCTTAATGGCCCTTGGACACCAAGATCTTTCCCATCTCTGTCCATG	1459
Db	1381	TCCCTCTGACCTCATATAACCTTAATGGCCCTTGGACACCAAGATCTTTCCCATCTCTGTCCATG	1440
Qy	1460	AATCATCTTCCCAACACAAATCAATCTATCTACTCACCTTAACAGCAACACTGGGGAGA	1519
Db	1441	AATCATCTTCCCAACACAAATCAATCTATCTACTCACCTTAACAGCAACACTGGGGAGA	1500
Qy	1520	GCCTGGAGCATCCGGACTTGCCCTTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1579
Db	1501	GCCTGGAGCATCCGGACTTGCCCTTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1560
Qy	1580	TCTGATTAATACAGACCTGTG	1600
Db	1561	TCTGATTAATACAGACCTGTG	1581

## RESULT 8

US-09-989-731-354  
; Sequence 354, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989, 731  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25



Db 841 GACCACCATCCACTCAGCCCTCTCTGGGTGCTTGTGGCTCTCTATACCCACTTCTGCTC 900  
Qy 920 CTGGACCTGTGAATAGTGGCAGCAGCAGCGGTTCTGCTGAACCTCCCTCTCTCA 979  
Db 901 CTGGACCTGTGAATAGTGGCAGCAGCAGCGGTTCTGCTGAACCTCCCTCTCTCA 960  
Qy 980 AGCTGCCCTGTCTCCAGGAGACGGCAGTGTCTCTACCTGTGTGAGCGGCTTGGAACTG 1039  
Db 961 AGCTGCCCTGTCTCCAGGAGACGGCAGTGTCTCTACCTGTGTGAGCGGCTTGGAACTG 1020  
Qy 1040 TTCAAGTGGCTCCCGGGAATGACCTCCCGAGGGGGCCCACTCATTTGTTATGATGGGTA 1099  
Db 1021 TTCAAGTGGCTCCCGGGAATGACCTCCCGAGGGGGCCCACTCATTTGTTATGATGGGTA 1080  
Qy 1100 CATTCATCTCTCAGGAGTGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159  
Db 1081 CATTCATCTCTCAGGAGTGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140  
Qy 1160 ACCTTCAGCTTCTTGTGTAACCAACACGACGAAATCGGGATCTTCTCTCGGGGTGAGAA 1219  
Db 1141 ACCTTCAGCTTCTTGTGTAACCAACACGACGAAATCGGGATCTTCTCTCGGGGTGAGAA 1200  
Qy 1220 GCGTGAATGACGCTCTCGCTCTCTAGCATGAGGAGGTGGGCTGAGGGCTGAGAGTC 1279  
Db 1201 GCGTGAATGACGCTCTCGCTCTCTAGCATGAGGAGGTGGGCTGAGGGCTGAGAGTC 1260  
Qy 1280 TCTCACTTGGGGGTGGGGCTGGCACTGGGCCCGAGCGCTGTGTGGGGAGTGGTTGCC 1339  
Db 1261 TCTCACTTGGGGGTGGGGCTGGCACTGGGCCCGAGCGCTGTGTGGGGAGTGGTTGCC 1320  
Qy 1340 TTCTCTGTAACCTATTATACCCCAACGATTTCTTACCGCTGTGACCAACCCACACTCAACC 1399  
Db 1321 TTCTCTGTAACCTATTATACCCCAACGATTTCTTACCGCTGTGACCAACCCACACTCAACC 1380  
Qy 1400 TCCTCTGACCTCATAACTTAATGGCTTGAGACACGATTTCTTCCACTTCTGTCCATG 1459  
Db 1381 TCCTCTGACCTCATAACTTAATGGCTTGAGACACGATTTCTTCCACTTCTGTCCATG 1440  
Qy 1460 AATCATCTTCCCAACACATCATTTATCTACTTACTTACTTACTTACTTACTTACTTACTT 1519  
Db 1441 AATCATCTTCCCAACACATCATTTATCTACTTACTTACTTACTTACTTACTTACTTACTT 1500  
Qy 1520 GCTTGGAGCATCGGACTTCCCTCTATGGGAGGGGAGCGCTGGAGGAGTGGCTGCGATGTA 1579  
Db 1501 GCTTGGAGCATCGGACTTCCCTCTATGGGAGGGGAGCGCTGGAGGAGTGGCTGCGATGTA 1560  
Qy 1580 TCTGATAATACAGACCTGTGTC 1600  
Db 1561 TCTGATAATACAGACCTGTGTC 1581

## RESULT 9

US-09-989-732-354  
; Sequence 354, Application US/09989732  
; Patent No. US20020123463A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C57  
; CURRENT APPLICATION NUMBER: US/09/989,732  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
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; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
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; PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090695  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090696  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090862  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/090863  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
;  
Query Match 98.7%; Score 1579.4; DB 3; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 20 CAGCCACAGACGGGTCTATGAGCGCGGTATTACTGTGGCCCTCTGGGGTTCTATCTCTCC 79  
DB 1 CAGCCACAGACGGGTCTATGAGCGCGGTATTACTGTGGCCCTCTGGGGTTCTATCTCTCC 60  
  
QY 80 ACTGCCAGGAGTGCAGGCGCTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAGGT 139  
DB 61 ACTGCCAGGAGTGCAGGCGCTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAGGT 120  
  
QY 140 GTCCGACCTGCCCGCAATGGACCCCTAAGAACACAGCTGCGACAGCGGCTTGGGGTG 199  
DB 121 GTCCGACCTGCCCGCAATGGACCCCTAAGAACACAGCTGCGACAGCGGCTTGGGGTG 180  
  
QY 200 CCAGGACAGTTGATGCTCTATTGAGAGCGGACCCCAAGTGAGCTGTGTCTCTCCAAGGG 259  
DB 181 CCAGGACAGTTGATGCTCTATTGAGAGCGGACCCCAAGTGAGCTGTGTCTCTCCAAGGG 240  
  
QY 260 CTGCACGAGGCGCAAGGACCCAGGAGCCCGCGTCACTGAGCACCCGATGGCCCCCGGCT 319  
DB 241 CTGCACGAGGCGCAAGGACCCAGGAGCCCGCGTCACTGAGCACCCGATGGCCCCCGGCT 300  
  
QY 320 CTCCTTGATCTCTACACCTTGTGTGCGCCAGGAGGACTTTCGAACAACCTCGTTAA 379  
DB 301 CTCCTTGATCTCTACACCTTGTGTGCGCCAGGAGGACTTTCGAACAACCTCGTTAA 360  
  
QY 380 CTCCTTCCGCTTTGGGCCCCCAGAGCCCCCAGAGCCCCAGAGATCTTTGAGGTGCCAGT 439  
DB 361 CTCCTTCCGCTTTGGGCCCCCAGAGCCCCCAGAGCCCCAGAGATCTTTGAGGTGCCAGT 420  
  
QY 440 CTGCTTGTCTATGGAAGGTGTCTGAGGGGACAAACAGAGAATCTTGCCCCCAAGGGGAC 499  
DB 421 CTGCTTGTCTATGGAAGGTGTCTGAGGGGACAAACAGAGAATCTTGCCCCCAAGGGGAC 480  
  
QY 500 CACACACTGTATGATGGGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCCATCTGAG 559  
DB 499 CACACACTGTATGATGGGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCCATCTGAG 559

Db 481 CACACACTGTTATGATGGCTCTCCTCAGGCTCAGGGAGGAGGCATCTTCTCCAATCTGAG 540  
Qy 560 AGTCCAGGATGATGAGCCAGCCAGGTTGCAACCTCTCTCAATGGGACACAGGAATGG 619  
Db 541 AGTCCAGGATGATGAGCCAGCCAGGTTGCAACCTCTCTCAATGGGACACAGGAATGG 600  
Qy 620 GCCCGTGGGTATGACTGAGAACTGCAATAGAAAGATTTTCTGACCTGTCTCATCGGGGAC 679  
Db 601 GCCCGTGGGTATGACTGAGAACTGCAATAGAAAGATTTTCTGACCTGTCTCATCGGGGAC 660  
Qy 680 CACATTTATGACACACAGAACTTGGCTCAAGAACCCCACTGATTTGGACCACTCAATAC 739  
Db 661 CACATTTATGACACACAGAACTTGGCTCAAGAACCCCACTGATTTGGACCACTCAATAC 720  
Qy 740 CGAGATGTCGAGTGGGGGAGGTGCTCAGGAGACCTGCTCTCATAGATGTAGACT 799  
Db 721 CGAGATGTCGAGTGGGGGAGGTGCTCAGGAGACCTGCTCTCATAGATGTAGACT 780  
Qy 800 CACATCAACCTTGTGGGGGACAAAGGCTGAGCACTGTTGGGGCTCAAAATTTCCCGAA 859  
Db 781 CACATCAACCTTGTGGGGGACAAAGGCTGAGCACTGTTGGGGCTCAAAATTTCCCGAA 840  
Qy 860 GACACACATCACTACGCCCTCTGGGGTGTGTCCTTATACCCACTTCTGCTC 919  
Db 841 GACACACATCACTACGCCCTCTGGGGTGTGTCCTTATACCCACTTCTGCTC 900  
Qy 920 CTGGACCTGTGCAATAGTGGCAGCAGCAGGCTTCTGCTGAACCTCCCTCTCTCTCA 979  
Db 901 CTGGACCTGTGCAATAGTGGCAGCAGCAGGCTTCTGCTGAACCTCCCTCTCTCTCA 960  
Qy 980 AGCTGCCCTGTGCCAGGACCGGAGTGTCTTACCTGTGTGCGAGCCCTTGAACCTG 1039  
Db 961 AGCTGCCCTGTGCCAGGACCGGAGTGTCTTACCTGTGTGCGAGCCCTTGAACCTG 1020  
Qy 1040 TTCAAGTGGCTCCCCCGAATGACCTGCCAGGGGCGCCACTCATTTGTTATGATGGGA 1099  
Db 1021 TTCAAGTGGCTCCCCCGAATGACCTGCCAGGGGCGCCACTCATTTGTTATGATGGGA 1080  
Qy 1100 CATTTCATCTCAGAGGTGGGTGTCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159  
Db 1081 CATTTCATCTCAGAGGTGGGTGTCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140  
Qy 1160 ACCTTCAGCTCTTGTGTTGAACACACAGACAAATCGGATCTTCTGCGCGTGAGAA 1219  
Db 1141 ACCTTCAGCTCTTGTGTTGAACACACAGACAAATCGGATCTTCTGCGCGTGAGAA 1200  
Qy 1220 GCGTGATGTGAGCCTCTGCTCTCAGCATGAGGGAGTGGGCTGAGGGCCTGGAGTC 1279  
Db 1201 GCGTGATGTGAGCCTCTGCTCTCAGCATGAGGGAGTGGGCTGAGGGCCTGGAGTC 1260  
Qy 1280 TCTCATTGGGGGTGGGGCTGGCACTGGGCCAGCGCTGTGTGGGGAGTGGTTTGGCC 1339  
Db 1261 TCTCATTGGGGGTGGGGCTGGCACTGGGCCAGCGCTGTGTGGGGAGTGGTTTGGCC 1320  
Qy 1340 TTCCTGCTTAATCTATTACCCACGATTTCTTACCCGCTGCTGACCCACCCACACTCAAC 1399  
Db 1321 TTCCTGCTTAATCTATTACCCACGATTTCTTACCCGCTGCTGACCCACCCACACTCAAC 1380  
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Db 1381 TCCCTCTGACCTCATAACTAATGGCTTGGACACAGATTTCTTTCCCATTTCTGCTCATG 1440  
Qy 1460 AATCATCTTCCGACACACAAATCTATATCTACTACCTAAACAGCAACACTGGGGAGA 1519  
Db 1441 AATCATCTTCCGACACACAAATCTATATCTACTACCTAAACAGCAACACTGGGGAGA 1500  
Qy 1520 GCTGGAGCATCCGAGCTTCCCTATGAGAGGGGAGCGCTGGAGGAGTGGCTCAGTGA 1579  
Db 1501 GCTGGAGCATCCGAGCTTCCCTATGAGAGGGGAGCGCTGGAGGAGTGGCTCAGTGA 1560  
Qy 1580 TCTGATTAATACAGACCTGTG 1600  
Db 1561 TCTGATTAATACAGACCTGTG 1581

## RESULT 10

US-09-991-073-354  
; Sequence 354, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730F1C15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
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; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
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; PRIOR APPLICATION NUMBER: 60/084600  
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; PRIOR APPLICATION NUMBER: 60/087106  
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, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/091982
, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

Query Match      98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      20  CAGCCACAGACGGGTTCATGAGCGCGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCCC 79
Db      1  CAGCCACAGACGGGTTCATGAGCGCGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCCC 60
Qy      80  ACTGCCAGGAGTGCAGCGCTGTCTGCCAGTTTGGACAGTTCAGCATGTGTGGAAGGT 139
Db      61  ACTGCCAGGAGTGCAGCGCTGTCTGCCAGTTTGGACAGTTCAGCATGTGTGGAAGGT 120
Qy      140  GTCCGACCTGCCCGCAATGGACCCCTTAAGACACAGCTGGACAGCGCTTGGGGTG 199
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Db 121 GTCCGACTACCCCGCAATGAGACCCCTAAGAAACACAGCTGCGACAGCGCTTTGGGGTG 180  
Qy 200 CCAGGACAGTTGATGCTCATTTAGAGCGGACCCCAAGTAGGCTGCTGCTCTCCCAAGGG 259  
Db 181 CCAGGACAGTTGATGCTCATTTAGAGCGGACCCCAAGTAGGCTGCTGCTCTCCCAAGGG 240  
Qy 260 CTGCA CGGAGGCAAGGACCAAGGACCGCGCTCACTGAGCACCGGATGGCCCCCGGCGCT 319  
Db 241 CTGCA CGGAGGCAAGGACCAAGGACCGCGCTCACTGAGCACCGGATGGCCCCCGGCGCT 300  
Qy 320 CTCCTGATCTCTACACTTCTGTTGTCGCGCAGGAGGACTTCTGCAACCAACTCTGTTAA 379  
Db 301 CTCCTGATCTCTACACTTCTGTTGTCGCGCAGGAGGACTTCTGCAACCAACTCTGTTAA 360  
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Qy 440 CTGCTTGTCTATGGAAGGCTGTCTGAGGGGACCAACAGAGAGATCTGCCCAAGGGGAC 499  
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Qy 500 CACACACTGTTATGATGCTCTCAGGCTCAGGGGAGGAGCATCTTCTCCAACTGAG 559  
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Qy 740 CGAGATGTGGAGTGGGGACGTTGCTCAGAGACGCTGCTCATAGATGAGACT 799  
Db 721 CGAGATGTGGAGTGGGGACGTTGCTCAGAGACGCTGCTCATAGATGAGACT 780  
Qy 800 CACATCAACCTGTGTGGGGCAAAAGGCTGCAGCACTGTTGGGCTCAAAATTTCCAGAA 859  
Db 781 CACATCAACCTGTGTGGGGCAAAAGGCTGCAGCACTGTTGGGCTCAAAATTTCCAGAA 840  
Qy 860 GACCACCATCACTCAGCCCCCTCTCGGGGTCTTGTGGCTCTCTATACCCCACTTCTGCTC 919  
Db 841 GACCACCATCACTCAGCCCCCTCTCGGGGTCTTGTGGCTCTCTATACCCCACTTCTGCTC 900  
Qy 920 CTGGACCTGTGCAATAGTCCAGCAGCAGCAGCGTTCTGCTGAACCTCCCTCCCTCTCA 979  
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Qy 980 AGCTGCCCTGTCTCCAGGACCGGAGTGTCTACCTGTGTGAGCGCTTGAACCTG 1039  
Db 961 AGCTGCCCTGTCTCCAGGACCGGAGTGTCTACCTGTGTGAGCGCTTGAACCTG 1020  
Qy 1040 TTCAAGTGGCTCCCCCGAATGACTGCCCGAGGGGCGCCACTCATTTGTTATGATGGGTA 1099  
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Qy 1100 CATTCATCTCTCAGAGGTGGCTGTCTCAACAAATAGCATTCAGGGCTGCGTGGCCCA 1159  
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## RESULT 11

US-09-990-442-354  
; Sequence 354, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730F1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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Query Match 98.7%; Score 1579.4; DB 3; Length 1587;  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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QY	140	GTCCGACCTGCC	CCGGCAATGACCCCTTAAGAACACACAGCTTGC	GACAGCGGCTTTGGGTTG	199
Db	121	GTCCGACCTTA	CCCCGGCAATGACCCCTTAAGAACACACAGCTTGC	GACAGCGGCTTTGGGTTG	180
QY	200	CCAGGACAGCTTG	TGCTCATTTGAGAGCGGACCCCAAGT	GAGCCTGTGTCTCTCCAAGG	259
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QY	260	CTGCA	CGGAGGCCAAGGACCAAGAGCCCGCGTCACTTG	AGCACGAGATGGGCCCGGCT	319
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QY	380	CTCCCTCCGCTTT	TGGGCCCCACAGCCCCAGCAGACCCAGGATCCTT	GAGTGGCCAGT	439
Db	361	CTCCCTCCGCTTT	TGGGCCCCACAGCCCCAGCAGACCCAGGATCCTT	GAGTGGCCAGT	420
QY	440	CTGCTTGCTTATG	GAAGGCTGTCTGTGGAGGGGACAACAGAAGAGATCT	GTGCCCCCAAGGGAC	499
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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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DB 181 CCAGGACAGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCTGTGTCTTCCAAGGG 240  
  
QY 260 CTGCAGGAGGCCAAGGACCCAGGAGCGCCCGCTCACTGAGCACCGGATGGGCCCGGCT 319  
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DB 301 CTCCTGTATCTCTACACCTTGTGTGCCCGCAGGAGGACTTCTGCAACACCTCTGTTAA 360  
  
QY 380 CTCCTCTCGCTTTGGGCCCCCAGGAGCGGACCCAGGATCCCTTGGAGTGGCCCGGCT 439  
DB 361 CTCCTCTCGCTTTGGGCCCCCAGGAGCGGACCCAGGATCCCTTGGAGTGGCCCGGCT 420  
  
QY 440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGAGAGATCTGCCCAAGGGGAC 499  
DB 421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGAGAGATCTGCCCAAGGGGAC 480  
  
QY 500 CACACATGTTATGATGGCTCTCTAGGCTCAGGGAGGAGGAGATCTTCTCCAATCTGAG 559  
DB 481 CACACATGTTATGATGGCTCTCTAGGCTCAGGGAGGAGGAGATCTTCTCCAATCTGAG 540  
  
QY 560 AGTCAGGAGTGCATGCCCGCAGGTTGCAACCTGCTCAATGGGACAGAGAAATGG 619  
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DB 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 660  
  
QY 680 CACCATTTAGACACACGGAAACTTTGGCTCAAGAACCCCACTGATGGACCAATGCAATAC 739  
DB 661 CACCATTTAGACACACGGAAACTTTGGCTCAAGAACCCCACTGATGGACCAATGCAATAC 720  
  
QY 740 CGAGATGTCGAGGTGGGGCAGGTGTGTCAGGAGCGCTGCTCTCATATGATGAGACT 799  
DB 721 CGAGATGTCGAGGTGGGGCAGGTGTGTCAGGAGCGCTGCTCTCATATGATGAGACT 780  
  
QY 800 CACATCAACCTCTGGTGAGCAAAAGGCTGACACACTGTTGGGGCTCAAAATTTCCAGAA 859  
DB 781 CACATCAACCTCTGGTGAGCAAAAGGCTGACACACTGTTGGGGCTCAAAATTTCCAGAA 840  
  
QY 860 GACCACCATCTCACTAGCCCTCTCTGGGGTGTGTTGGGCTCTCTATACCACTTCTGCTC 919  
DB 841 GACCACCATCTCACTAGCCCTCTCTGGGGTGTGTTGGGCTCTCTATATACCACTTCTGCTC 900

Qy	920	CTCGGACCTGTGCMAATAGTGTCCAGCAGCAGGAGCGTTCTGCTGAACCTCCCTCCCTCCTCA	979
Db	901	CTCGGACCTGTGCAATAGTGTCCAGCAGCAGCAGCGTTCTGCTGAACCTCCCTCCCTCCTCA	960
Qy	980	AGCTGCCCTGTGCCAGGAGACCGCAGTGTCTTACCTGTGTGCAGGCCCTTGGAACTCG	1039
Db	961	AGCTGCCCTGTGCCAGGAGACCGCAGTGTCTTACCTGTGTGCAGGCCCTTGGAACTCG	1020
Qy	1040	TTCAAGTGGCTTCCCCCGAATGACCTGCCGCCAGGGGCGCCACTCATTTGTTATGATGGGTA	1099
Db	1021	TTCAAGTGGCTTCCCCCGAATGACCTGCCGCCAGGGGCGCCACTCATTTGTTATGATGGGTA	1080
Qy	1100	CATTTCATCTCTCAGGAGGTGGCTGTCCACCACCAATGAGCATTCAGGGCTGCGTGGCCCCA	1159
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Qy	1160	ACCTTCCAGCTTCTTGTGTGAACCAACACAGACAAATCGGGATCTTCTGCGGTGAGAA	1219
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Qy	1220	GGCTGATGTGCAGCCTCCTGCCCTCTCAGCATGAGGAGGTGGGGCTGAGGGCCTGGAGTC	1279
Db	1201	GGCTGATGTGCAGCCTCCTGCCCTCTCAGCATGAGGAGGTGGGGCTGAGGGCCTGGAGTC	1260
Qy	1280	TCTCACTTGGGGGGTGGGGCTGGCACCTGGGCCCAACGCGCTGTGTGGGGAGTGTGTTGCC	1339
Db	1261	TCTCACTTGGGGGGTGGGGCTGGCACCTGGGCCCAACGCGCTGTGTGGGGAGTGTGTTGCC	1320
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## RESULT 15

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US-09-989-721-354
Sequence 354, Application US/099898721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavins, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.

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;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
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Best Local Similarity 99.9%; Pred. No. 0;  
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Qy	260	CTGCACGGAGGCCAAGGACCCAGGAGCCCGCTCACTGAGCACCGGATGGCGCCCGGCT	319
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Qy	320	CTCCCTGATCTCTTACACCTTGTGTGCGCGCAGGAGGACTTCTGCAACAACTCTGTTAA	379
Db	301	CTCCCTGATCTCTTACACCTTGTGTGCGCGCAGGAGGACTTCTGCAACAACTCTGTTAA	360
Qy	380	CTCCCTCCCGCTTGGGCCCCCAGAGCCCGGAGCCAGGATCTTGAAGTCCCAAGT	439
Db	361	CTCCCTCCCGCTTGGGCCCCCAGAGCCCGGAGCCAGGATCTTGAAGTCCCAAGT	420
Qy	440	CTGCTTGTCTATGGAAGCTGTCTTGGAGGGGACAAACAGAGAGATCTGCCCAAGGGAC	499
Db	421	CTGCTTGTCTATGGAAGCTGTCTTGGAGGGGACAAACAGAGAGATCTGCCCAAGGGAC	480
Qy	500	CACACACTGTATGATGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCAATCTGAG	559
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Search completed: July 11, 2006, 11:23:08  
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DB 541 AGTCCAGGATGATGCCCGAGCCAGGTTGCAACTGCTCAATGGGACACAGGAATTGG 600  
QY 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGAATTTCTGACCTGTCTATCGGGGAC 679  
DB 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGAATTTCTGACCTGTCTATCGGGGAC 660  
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QY 800 CACATCAACCTGTGGGGACAAAGGCTGCAGCACTGTGGGGCTCAAAATTTCCAGAA 859  
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GenCore version 5.1.9  
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Listing first 45 summaries

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13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	991	61.9	1048	1	AL545603
4	928.8	58.1	986	5	CD514938
5	898.2	56.1	1043	1	AL543219
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8	816	51.0	883	4	EX371592
9	809.4	50.6	923	1	AL543254
10	754.4	47.1	894	2	BI758869
11	736	46.0	883	4	EX371593
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13	685.8	43.5	766	9	DA728784
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40	568.4	35.5	570	9	DA427412	DA427412
41	568.4	35.5	570	9	DA430759	DA430759
42	568.4	35.5	571	1	AU310872	AU310872
43	567.6	35.5	574	3	BP221450	BP221450
44	567.4	35.5	569	9	DA428316	DA428316
45	566.8	35.4	570	9	DA878296	DA878296

## ALIGNMENTS

### RESULT 1

CR592446

LOCUS

DEFINITION

full-length cDNA clone CSODI015Y017 of Placenta Cot 25-normalized

of Homo sapiens (human).

ACCESSION

CR592446

VERSION

CR592446.1 GI:50473253

KEYWORDS

HTC; CNSUT\_CDNA.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 2146)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

REFERENCE

2 (bases 1 to 2146)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

FEATURES

Location/Qualifiers

source

1. .2146

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODI015Y017"

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/plasmid="pCMVSPORT\_6"

ORIGIN

Query Match

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Qy	81	CTGCCAGGAGTGCAGGGCGCTGCTCTGCCAGTTTGGGACAGTTACGACATGTTGGAAGGTG	140
Db	61	CTGCCAGGAGTGCAGGGCGCTGCTCTGCCAGTTTGGGACAGTTACGACATGTTGGAAGGTG	120
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Db	421	TGCTTGTCTATGGAAGGCTCTCTGGAGGGGACACAGAGAGATCTGCCCCAGGGGACC	480
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Qy	561	GTCAGGAGTGTCATGCCACGACGTTGCAACCTGCTCAATGGGACACAGGAATTTGGG	620
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Qy	621	CCCGTGGGTATGACTGAGAACTGCAATAGGAAGAATTTCTGACCTGTCTATCGGGGACC	680
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Qy	681	ACCATTATGACACGGAACCTTGGCTCAAGAACCCCACTGATGGGACCAATCGAATACC	740
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Qy	741	GAGATGTGCGAGTGGGGCAGGTGTCTCAGGAGACGCTGCTGCTCATAGATGTAGGACTC	800
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Qy	981	GCTGCCCTGTGCCAGGAGACCGCAGTGTCTACTGTGTGTCAGCCCCCTTGGAACTGT	1040
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DB 361 CCCACAGCCCGCAGCAGACCCAGGATCTTGGAGTGGCCAGTCTGCTTGTCTATGGAAG 420  
  
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DB 541 CCAGCCAGTTTGCACCTGCTCAATGGGACACAGGAAATTTGGGCGCCGTTGGTATGACTGA 600  
  
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QY 1538 TGCCCTATGGAGGGGAGCGCTGGAGAGTGGTGTGCTATCTGATTAATACAG 1592  
DB 1501 TGCCCTATGGAGGGGAGCGCTGGAGAGTGGTGTGCTATCTGATTAATACAG 1555  
  
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LOCUS  
DEFINITION  
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Clone CS0D1015Y017 5-PRIME, mRNA sequence.  
ACCESSION  
AL545603  
VERSION  
AL545603.3 GI:45746083  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1048)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31267438.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9230.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?8=CS0D1015AH09Q1&c=9230.r.
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		/note="1st strand cDNA was primed with a NotI-oligo(dT)	
		primer. Five prime end enriched, double-strand cDNA was	
		digested with Not I and cloned into the Not I and EcoR V	
		sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN			
Query Match		61.9%; Score 991; DB 1; Length 1048;	
Best Local Similarity		97.9%; Pred. No. 6.4e-249;	
Matches 1025; Conservative		0; Mismatches 20; Indels 2; Gaps 2;	
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DB	181	CAGGACAGCTTGATGCTCATGTAGAGCGGACCCCAAGTGAGCCTGTGCTCTCCAAAGGCG	240
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DB	301	TCCTCATCTCTTACACCTTGTGTGCGCCGAGGAGACTTCTGCAACACCTCGTTAAC	360
QY	381	TCCTCCCGGTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTCTGAGGTGCCAGTGC	440
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QY	980	AGCTGCCCTGTCCAGGAGACCGCAGTGTCTTACCTGTGTGACGCCCTTGGAACTGT	1039
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QY	1040	TTCAAGTGGCTCCCGCCGAATGACCTG	1066
DB	1020	TGATGGCTCCCGAATGACTGCCAG	1046
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CD514938		986 bp mRNA linear EST 06-JUN-2003	
LOCUS		AGENCOURT 14368747 NIH_MGC_181 Homo sapiens cDNA clone	
DEFINITION		IMAGE:30408929 5', mRNA sequence.	
ACCESSION		CD514938	
VERSION		CD514938.1 GI:31446656	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
		Hominidae; Homo.	
REFERENCE		1 (bases 1 to 986)	
AUTHORS		NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a>	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: gcapbs-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDAM492 row: k column: 18 High quality sequence stop: 710.	
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ORIGIN			
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Best Local Similarity		96.9%; Pred. No. 1.4e-232;	
Matches 956; Conservative		0; Mismatches 30; Indels 1; Gaps 1;	
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Db 121 CCGCAATAGACCCCTTAAGAACACACAGCTGCGACAGCGGCTTGGGTGCGCAGGACAGTT 180
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Db 841 CTCAGCCCTCTCTGGGCTGTGTGGCTCTCTATACCCACTTCTGCTCTCGGACCTGTG 900
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QY 932 CAATAGTGCAGACGACGCTGTGCTGAACTCCCTCTCTCAAGTGCCTCTGT 991
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Db 901 CAATAGTGCAGACGACGCTGTGCTGAACTCCCTCTCTCAAGTGCCTCTGT 959
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Db 960 CCCAGGACCGGAGTGTCTTACTG 986
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DEFINITION AL543219 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1001YG18 3-PRIME, mRNA sequence.
ACCESSION AL543219
VERSION AL543219.3 GI:45718783
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**KEYWORDS**  
**SOURCE**  
**ORGANISM**

EST.  
Homo sapiens (human)  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

**REFERENCE**

1 (bases 1 to 1043)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

**TITLE**

Unpublished (2001)

**JOURNAL**

COMMENT

On Feb 15, 2001 this sequence version replaced gi:31265066.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqraf@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

9230.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0D1001BD09NP1&c=9230.r.

Location/Qualifiers

1. .1043

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/db\_xref="taxon:9606"

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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with NotI and cloned into the NotI and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 56.1%; Score 898.2; DB 1; Length 1043;

Best Local Similarity 97.9%; Pred. No. 1.6e-24;

Matches 923; Conservative 4; Mismatches 14; Indels 2; Gaps 2;

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Db 941 GAAAGATTTTCTGACCTGTCTATCGGGGACCCACCATTTATGACACACGGAATCTTGCTCA 883

QY 710 AGAACCACCTGATTGGACCAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 769

Db 882 AGAACCACCTGATTGGACCAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCA 823

QY 770 GGAGACCTGCTGCTCATAGATGTAGACTCAGATCAACCTGCTGGGACAAAAGGCTG 829

Db 822 GGAGACCTGCTGCTCATAGATGTAGACTCAGATCAACCTGCTGGGACAAAAGGCTG 763

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Db 762 CAGACCTGTTGGGGCTCAAAATTTCCAGAGACCCACCATCCACTCAGCCCTCTCTGGGGT 703

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QY 1070 CAGGGGCGCCACTATGTTTATGATGGTACATTCATCTCTCAGAGAGTGGGCTGTCCAC 1129

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QY 1130 CAAATGAGCAATTCAGGCTGGTGGCCCAACCTCCAGCTTCTTGTGAACACACACAG 1189  
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Db 462 CAAATGAGCAATTCAGGCTGGTGGCCCAACCTCCAGCTTCTTGTGAACACACACAG 403  
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QY 1550 GAGGGAGCGTGAGAGTGGCTGCATGTATCTGTAATATACAG 1592  
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## RESULT 6

BQ894891  
LOCUS AGENCOURT\_8616434 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6302444  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ894891  
VERSION BQ894891.1 GI:22286905  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 901)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCW2519 row: 0 column: 21  
High quality sequence stop: 647.  
Location/Qualifiers

## FEATURES

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/clone\_lib="NIH\_MGC\_113"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Library constructed by Ling Hong in the

## ORIGIN

Query Match 52.5%; Score 840.8; DB 3; Length 901;  
Best Local Similarity 98.7%; Pred. NO. 1.9e-209;  
Matches 889; Conservative 0; Mismatches 8; Indels 4; Gaps 4;  
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QY 1004 G 1004  
Db 900 G 900

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RESULT 7
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LOCUS
DEFINITION
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IMAGE:7471271 5', mRNA sequence.
CX167363
ACCESSION
CX167363.1 GI:56797443
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 827)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-x@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15774 Row: 1 Column: 21
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 827.
Location/Qualifiers
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an early endodermal cell type"
/cell_type="human embryonic stem cells"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH MGC 258"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Positive for
GATA4, Mixl1, Mx1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGGCGCGGCCCTTT25-3', and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH MGC 259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."
ORIGIN
Query Match 51.68; Score 825.4; DB 8; Length 827;
Best Local Similarity 99.99; Pred. No. 2.1e-205;
Matches 826; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 20 CAGCCACAGCGGTCATGAGCGGGTATTACTGCTGGCCCTCTCTGGGGTTTCATCTCCC 79
Db 1 CAGCCACAGCGGTCATGAGCGGGTATTACTGCTGGCCCTCTCTGGGGTTTCATCTCCC 60

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Qy 80 ACTGCCAGGAGTCAGGCGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGT 139
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Qy 140 GTCCGACCTGCCCGGCAATGGACCCCTAAGAAACACCAAGTCGACAGCGCTTTGGGGTG 199
Db 121 GTCGACCTGCCCGGCAATGGACCCCTAAGAAACACCAAGTCGACAGCGCTTTGGGGTG 180
Qy 200 CAGGACACCTTGATGCTCTATTGAGAGCGGACCCCAAGTAGAGCTGTCTCTCAAGGG 259
Db 181 CCAGGACACCTTGATGCTCTATTGAGAGCGGACCCCAAGTAGAGCTGTCTCTCAAGGG 240
Qy 260 CTGCACGAGGCGCAAGGACCAAGGAGCCCGCGTCACTGAGCACCGGATGGCCCGCGCT 319
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Qy 320 CTCCTTGATCTCTACACCTTTCGCTGTCGCCAGGAGGACTTTGCAACACCTCGTTAA 379
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Qy 380 CTCCTTCCCGCTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGTGGCCAGT 439
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Qy 680 CACCATTTATGACACACGAAACTTGGCTCAAGAACCCCACTGATTGGACCAATCGAATAC 739
Db 661 CACCATTTATGACACACGAAACTTGGCTCAAGAACCCCACTGATTGGACCAATCGAATAC 720
Qy 740 CGAGATGTCGAGGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCATAGATGAGACT 799
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Db 781 CACATCAACCTGTTGGGGACAAAGGCTGCAGCAGCTGTTGGGGCTC 827

RESULT 8
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DEFINITION
BX371592 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI015Y017 3-PRIME, mRNA sequence.
ACCESSION
BX371592
VERSION
BX371592.2 GI:46625729
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 883)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30456041.
Contact: Genoscope

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Qy 158 ATGACCCCTAAGAACACACAGCTCGACAGCGGCTTGGGTGCCAGGACAGCTTGATGCT 217
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Qy 818 GACAAAGGCTGACGACTGTTGGGGCTCAAAATTTCCAGAGACACCATCTCATCAGC 877
Db 781 GACAAA--GGCTGCRCACTGTTGGGGCTCAAAATTTCCAGAGAG--CAACATCCACTCAG- 836
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RESULT 10
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DEFINITION 603042311F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182826 5',
mRNA sequence.
ACCESSION BI758869
VERSION BI758869.1 GI:15750447
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11456 row: e column: 03  
High quality sequence stop: 869.  
Location/Qualifiers  
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/clone="IMAGE:5182826"  
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/clone\_lib="NIH\_MGC\_116"  
/notes="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH\_MGC Library."

## ORIGIN

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Query Match 47.1%; Score 754.4; DB 2; Length 894;  
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Db 540 AGAGTCCAGGAGTGCATGCCGCCAGCGAGTTGCAACCTGCTCAATGGGACACAGAAATT 599
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**AUTHORS**  
Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
Mewes, H.W., Wei, B., Amd, C., Osanger, A., Fobo, G., Han, M. and  
Wiemann, S.

**TITLE**  
EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,  
Wellenreuther, R., et al.)

**JOURNAL**  
Unpublished (2003)

**COMMENT**  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp781B2333) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

**FEATURES**  
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cDNA-collection"

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Query Match 44.1%; Score 705.4; DB 4; Length 729;  
Best Local Similarity 99.2%; Pred. No. 7.2e-174;  
Matches 709; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAAAGCAGAAGAGATTACCAAGCGGTCATGAGCGCGTATTACTGCTGGCCC 60  
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DB 369 TCTCAACAACCTGTTAACTCCCTCCGCTTGGGCGCCACAGCCCGCCAGCACGCCAG 428  
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DB 489 AGATCTGCCCCAAGGGACACACACTGTTATGATGGCTCTCTCAGGCTCAGGGAGAG 548  
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LOCUS DA728784 766 bp mRNA linear EST 11-NOV-2005  
DEFINITION DA728784 NT2RM2 Homo sapiens cDNA clone NT2RM2002461 5', mRNA  
sequence.  
ACCESSION DA728784  
VERSION DA728784.1 GI:81802098  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 766)  
AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,  
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,  
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,  
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,  
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,  
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560  
Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com  
NEDO human cDNA project (New Energy and Industrial Technology  
Developmental Organization, Japan); cDNA library construction:  
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,  
Research Association for Biotechnology (RAB) and Biotechnology  
Center, National Institute of Technology and Evaluation; 3'-end one  
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**ORIGIN**  
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Best Local Similarity 99.1%; Pred. No. 2.4e-171;  
Matches 734; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

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QY 61 TCCTGGGGTTTCATCTCCCACTGCCAGAGTGCAGGCGCTCTCTGCCAGTTTGGACAG 120



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Db      142  TTCCAGATCTGTGGAGGTGTCGACCTCGCCCGCAATGAGACCCCTTAAGAACACACAGCT 201
Qy      181  GGCACAGCGGCTTGGGGTGCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGA 240
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Qy      481  AGATCTGCCCCCAAGGGACACACACTGTTATGATGSCCTCTCAGGCTCAGGGGAGGAG 540
Db      502  AGATCTGCCCCCAAGGGACACACACTGTTATGATGSCCTCTCAGGCTCAGGGGAGGAG 561
Qy      541  GCATCTTCTCCAACTCAGAGTCAGGGATGCAATGCCCCAGCCAGGTTGCAACTGCTCA 600
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Db      739  GATTGGACACATCGAATACCGAATGT 766
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LOCUS
DEFINITION 5605468071 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630132
VERSION CD630132.1 GI:40278398
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 727)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
PUBMED 15203218
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..727
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Best Local Similarity 98.5%; Pred. No. 4.3e-162;
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Qy      988  CTGTCCAGGAGACCGGCACTGTCTTACCTGTGTGCAGCCCTTTGGAACCTGTTCAGTG 1047
Db      121 CTGTCCAGGAGACCGGCACTGTCTTACCTGTGTGCAGCCCTTTGGAACCTGTTCAGTG 180
Qy      1048  GCTCCCCCGAATGACTGCCCGAGGCGCCACTCATTTGTTATGATGGGTACATTCATC 1107
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Db      300 GCTTTTGTGTGAACCAACACAGCAAAATCGGGAATCTTCTCTGCGCGTGAGAGCGTGATG 359
Qy      1228  TGCAGCTCTCTGCTCTCAGCATGAGGAGTGGGCTGAGGGCTGGAGTCTCTCACTT 1287
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Qy      1288  GGGGGTGGGGCTGGGCACTGGGCCCGAGCGCTGTGTGGGAGTGGTTGGCTTCCTGCT 1347
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Qy      1408  ACCTCATACCTTAATGGCTTGGACACAGATTTCTTCCCATTTCTGTCCATGATCATCT 1467
Db      540 ACCTCATACCTTAATGGCTTGGACACAGATTTCTTCCCATTTCTGTCCATGATCATCT 599
Qy      1468  TCCCCACACACATCATTTATCTACTACTACCTAAACAGCAACACTGGGG--AGAGCTCG 1525
Db      600 TCCCCA-ACACATCATTTATCTACTACTACCTAAACAGCAACACTGGGGAGAGCTCG 658
Qy      1526  AGCATCCGGAC-TTGGCCCTATGGAGAGGGACGCTGGAGGAGTGGCTGATGATCTGA 1584
Db      659 AGCANGCGGACTTTGCCCTATGGAGAGGGACGCTGGAGAGTGG-TGCATGTATCTGA 717
Qy      1585  TAATACAGAC 1594
Db      718 TAATACAGAC 727
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RESULT 15
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LOCUS
DEFINITION 8426 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC029167, mRNA sequence.
ACCESSION CV029587
VERSION CV029587.1 GI:51487767
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

# REFERENCE AUTHORS

Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Guisick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press

# TITLE JOURNAL COMMENT

Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu  
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

# PCR Primers

FORWARD: ATGAGCCCGGTATTACTG

BACKWARD: TAGCAGAGGCGCAACCA

Insert Length: 627 Std Error: 53.00

Plate: 11036 row: 06 column: G

Seq primer: ATGGCCGCTGTTTACACGTCGTGACTGGGAAAC

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POLYA=No.

# FEATURES source

Location/Qualifiers  
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/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

# ORIGIN

Query Match 38.9%; Score 621.8; DB 8; Length 627;  
Best Local Similarity 99.4%; Pred. No. 6.6e-152;  
Matches 623; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 96 GCGCTGCTCTCCAGTTGGGACAGTTTCAGCATGTGTGGAGTGTCCGACCTGCCCGG 155  
Db 61 GCGCTGCTCTCCAGTTGGGACAGTTTCAGCATGTGTGGAGTGTCCGACCTGCCCGG 120

Qy 156 CAATGGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTCCAGGACACGTTGATG 215  
Db 121 CAATGGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTCCAGGACACGTTGATG 180

Qy 216 CTCAATTGAGAGCGGACCCCAAGTGAAGCTGTGTCTTCAAGGGCTGCACGGAGGCCAAG 275  
Db 181 CTCAATTGAGAGCGGACCCCAAGTGAAGCTGTGTCTTCAAGGGCTGCACGGAGGCCAAG 240

Qy 276 GACCAGAGCCCGCGTCACTGACACCGGATGGGCGCCGCTCTCCCTGATCTCTTAC 335  
Db 241 GACCAGAGCCCGCGTCACTGACACCGGATGGGCGCCGCTCTCCCTGATCTCTTAC 300

Qy 336 ACCTTCGTGTGTCGCCAGGAGGACTTCTGCAACAACTCGTTAACTCCCTCCCGCTTTGG 395

Db 301 ACCTTCGTGTGTCGCCAGGAGGACTTCTGCAACAACTCGTTAACTCCCTCCCGCTTTGG 360  
Qy 396 GCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGAA 455  
Db 361 GCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGAA 420  
Qy 456 GGCTGTCTGAGGGGCAACACAGAAAGAGATCTGCCCAAGGGGACACACACTGTTATGAT 515  
Db 421 GGCTGTCTGAGGGGCAACACAGAAAGAGATCTGCCCAAGGGGACACACACTGTTATGAT 480  
Qy 516 GGCTTCCTCAGGCTCAGGGGAGGAGGCAATCTTCTCAATCTGAGAGTCCAGGGGATGATG 575  
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Qy 576 CCCAGCCAGGTTGCAACTGCTCTCAATGGGACACAGGAAATTTGGCCCGTGGGTATGACT 635  
Db 541 CCCAGCCAGGTTGCAACTGCTCTCAATGGGACACAGGAAATTTGGCCCGTGGGTATGACT 600  
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1579.4	98.7	1587	3	US-10-033-301-15
5	1579.4	98.7	1587	3	US-09-997-333-354
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8	1579.4	98.7	1587	4	US-09-989-735-354
9	1579.4	98.7	1587	5	US-09-989-726-354
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16	913	57.1	1311	3	US-09-073-569-4
17	436.6	27.3	450	3	US-09-621-976-396
18	345.4	21.6	370	3	US-09-023-655-287
19	171.2	10.7	211	3	US-09-471-276-104
20	50	3.1	408	3	US-09-513-999C-28111
21	48.4	3.0	1170	3	US-09-902-540-8353
22	48.4	3.0	8056	3	US-09-902-540-874
23	45.2	2.8	508	3	US-09-621-976-3248

#### ALIGNMENTS

##### RESULT 1

US-09-830-189C-1

; Sequence 1, Application US/09830189C

; Patent No. 6686153

; GENERAL INFORMATION:

; APPLICANT: PAHL, HEIKE

; TITLE OF INVENTION: PRV-1 AND THE USE THEREOF

; FILE REFERENCE: LEDER-1

; CURRENT APPLICATION NUMBER: US/09/830,189C

; CURRENT FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: PCT/EP99/07238

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 198 49 044.5

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; TYPE: DNA

; ORGANISM: Homo sapiens

; LENGTH: 1600

US-09-830-189C-1

Query Match 100.0%; Score 1600; DB 3; Length 1600;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAGCAGAAAGAGATTACCAGCCACAGAGCGGTCTATGAGCGCGGTATTACTGTGCCCC 60

QY 61 TCCTGGGGTTTCATCTCCCACTGCCAGGAGTGAGCGGCTGCTCTGCCAGTTTGGGACAG 120

Db 61 TCCTGGGGTTTCATCTCCCACTGCCAGGAGTGAGCGGCTGCTCTGCCAGTTTGGGACAG 120

QY 121 TTCAGCATGTGTGGAAGGTGTCGACCTCCCGGCAATGGAACCCCTTAACAACACCAAGCT 180

Db 121 TTCAGCATGTGTGGAAGGTGTCGACCTCCCGGCAATGGAACCCCTTAACAACACCAAGCT 180

QY 181 GCACAGCGGCTGGGGTGCAGGACACGTTGATGTCTATTGAGAGCGGACCCCAAGTGA 240

Db 181 GCACAGCGGCTGGGGTGCAGGACACGTTGATGTCTATTGAGAGCGGACCCCAAGTGA 240

QY 241 GCCTGTGTCTTCCAAAGGCTGCACGGAGCCCAAGGACCCCGGTCACCTGAGC 300

Db 241 GCCTGTGTCTTCCAAAGGCTGCACGGAGCCCAAGGACCCCGGTCACCTGAGC 300

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Sequence 1379, Ap  
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Sequence 13, Appl  
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Sequence 108, App  
Sequence 122, App  
Sequence 15180, A  
Sequence 14922, A  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 14, Appl  
Sequence 1963, Ap  
Sequence 2047, Ap  
Sequence 1909, Ap  
Sequence 42, Appl

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QY	80	ACTGCCAGAGTGCAGGCGCTCTCTGCCAGT	TTGGGACAGTTTCAGCATGTGTGGAGGT	139			
DB	61	ACTGCCAGAGTGCAGGCGCTCTCTGCCAGT	TTGGGACAGTTTCAGCATGTGTGGAGGT	120			
QY	140	GTCCGACCTGCCCCGCAATAGACCCCTTA	AGAACACCAAGCTGCGACAGCGGCTTGGGGTG	199			
DB	121	GTCCGACCTGCCCCGCAATAGACCCCTTA	AGAACACCAAGCTGCGACAGCGGCTTGGGGTG	180			
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DB	241	CTGCAGGAGGCCAAGGACCAAGGACCG	CGCTCACTGAGCACCGGATGGCCCGGCT	300			
QY	320	CTCCCTGATCTCTACACCTTCGTGTGCC	CCGACAGGAGCTTCTGCAACAACCTCGTTAA	379			
DB	301	CTCCCTGATCTCTACACCTTCGTGTGCC	CCGACAGGAGCTTCTGCAACAACCTCGTTAA	360			
QY	380	CTCCCTCCGCTTTGGGCCCCACAGCCCC	CCAGCAGACCCAGGATGGGCTGCCAGT	439			
DB	361	CTCCCTCCGCTTTGGGCCCCACAGCCCC	CCAGCAGACCCAGGATGGGCTGCCAGT	420			
QY	440	CTGCTTGCTATNGAAGGCTGTCTGAGG	GGGACCAAGAGAGATCTGCCCAAGGGAC	499			
DB	421	CTGCTTGCTATNGAAGGCTGTCTGAGG	GGGACCAAGAGAGATCTGCCCAAGGGAC	480			
QY	500	CACACACTGTATATGATGGCTCTCTC	AGGCTCAGGGGAGGAGCATCTTCTCCAATCTGAG	559			
DB	481	CACACACTGTATATGATGGCTCTCTC	AGGCTCAGGGGAGGAGCATCTTCTCCAATCTGAG	540			
QY	560	AGTCCAGGATGATGCCCGCAGCCAGG	TTGCAACCTGCTCATTTGGGACACAGAAATGG	619			
DB	541	AGTCCAGGATGATGCCCGCAGGTTTG	CAACCTGCTCAATTGGGACACAGAAATGG	600			
QY	620	GCCCGTGGGTATGACTGAGAACTGCA	ATAGGAAGATTTTCTGACCTGTCTCGGGGAC	679			
DB	601	GCCCGTGGGTATGACTGAGAACTGCA	ATAGGAAGATTTTCTGACCTGTCTCGGGGAC	660			
QY	680	CACATTATGACACACGGAACCTTGG	CTCAAGAACCCACTGATTGGACCAACATCGAATAC	739			
DB	661	CACATTATGACACACGGAACCTTGG	CTCAAGAACCCACTGATTGGACCAACATCGAATAC	720			
QY	740	CGAGATGTGGAGGTGGGCGAGGTGT	CTCAGGACGCTGCTCTCATGATGTAGACT	799			
DB	721	CGAGATGTGGAGGTGGGCGAGGTGT	CTCAGGACGCTGCTCTCATGATGTAGACT	780			
QY	800	CACATCAACCTTGGTGGGACAAAG	CGTGCAGCACTTTGGGGCTCAAAATTTCCAGAA	859			
DB	781	CACATCAACCTTGGTGGGACAAAG	CGTGCAGCACTTTGGGGCTCAAAATTTCCAGAA	840			
QY	860	GACCAACCTCACTAGCCCCCTCTG	GGGTGCTTTGGCCCTCTATACCACCTTCTGCTC	919			
DB	841	GACCAACCTCACTAGCCCCCTCTG	GGGTGCTTTGGCCCTCTATACCACCTTCTGCTC	900			
QY	920	CTCGGACCTGTGCAATAGTGCAG	CGACAGCAGCTTCTGCTGAATCCCTCCCTCTCA	979			
DB	901	CTCGGACCTGTGCAATAGTGCAG	CGACAGCAGCTTCTGCTGAATCCCTCCCTCTCA	960			
QY	980	AGCTGCCCTGTCCCAAGGACCGG	AGTGTCTTACTGTGTGAGCCCTTGGAACTTG	1039			
DB	961	AGCTGCCCTGTCCCAAGGACCGG	AGTGTCTTACTGTGTGAGCCCTTGGAACTTG	1020			
QY	1040	TTCAAATGGGCTCCCCCGAATGAC	CTGTGCCCCAGGGGCGCCACTCAATGTGTTATGATGGGTA	1099			

Db	1021																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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RESULT 3

US-09-990-444-354  
; Sequence 354, Application US/09990444  
; Patent No. 6930170

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C19  
; CURRENT APPLICATION NUMBER: US/09/990,444





; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGCCACAGACGGGTATGAGCGCGGTATTAATCTGCTGGCCCTCTGGGTTTCACTCTCCC 79
DB 1 CAGCCACAGACGGGTATGAGCGCGGTATTAATCTGCTGGCCCTCTGGGTTTCACTCTCCC 60

QY 80 ACTGCCAGAGTGCAGCGCTGCTCTGCCAGTTTGGGACAGTTGACATGTGGAAGT 139
DB 61 ACTGCCAGAGTGCAGCGCTGCTCTGCCAGTTTGGGACAGTTGACATGTGGAAGT 120

QY 140 GTCGACCTGCCCGGCAATGGAACCCCTAAGAACACCAAGTGCAGCAGCGGCTTGGGGTG 199
DB 121 GTCGACCTTACCCCGCAATGGACCCCTAAGAACACCAAGTGCAGCAGCGGCTTGGGGTG 180

QY 200 CAGGACAGCTTATCTCATTTGAGAGCGGACCCCAAGTGAAGCTGCTCTCCAAAGG 259
DB 181 CAGGACAGCTTATCTCATTTGAGAGCGGACCCCAAGTGAAGCTGCTCTCCAAAGG 240

QY 260 CTGACGAGGCGCAAGACCAAGAGCCCGCGCTCACTGAGCACCGGATGGGCCCCCGGCT 319
DB 241 CTGACGAGGCGCAAGACCAAGAGCCCGCGCTCACTGAGCACCGGATGGGCCCCCGGCT 300

QY 320 CTCCTCTGATCTCTACACCTTCTGTCGCGCCAGGAGGACTTCTGCAACAACTCGTTAA 379
DB 301 CTCCTCTGATCTCTACACCTTCTGTCGCGCCAGGAGGACTTCTGCAACAACTCGTTAA 360

QY 380 CTCCTCTGCTTGGGCCCCCAGCCCCCAGAGCCAGGATCTTGAAGTGGCCAGT 439
DB 361 CTCCTCTGCTTGGGCCCCCAGCCCCCAGAGCCAGGATCTTGAAGTGGCCAGT 420

QY 440 CTCCTTGTCTATGGAAGGCTGCTGAGAGGGAACAAGAGAGATCTGCCCAAGGGGAC 499
DB 421 CTCCTTGTCTATGGAAGGCTGCTGAGAGGGAACAAGAGAGATCTGCCCAAGGGGAC 480

QY 500 CACACATGTTATGAGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCAACTCTGAG 559
DB 481 CACACATGTTATGAGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCAACTCTGAG 540

QY 560 AGTCCAGGATGATGCCCCAGCGGTTGCAACCTGCTCAATGGGACACAGAAATGG 619
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QY 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 679
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QY 680 CACCATTAACACAGGAAACTTGGCTAAGAACCCCACTGATTTGGACCACTCGAATAC 739

DB 661 CACCATTAACACAGGAACTTGGCTCAAGAACCCACTGATGGACCACTCGAATAC 720
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DB 721 CGAGATGTGCGAGGTGGGCGAGGTGTGTCAGAGAGCGCTGCTCATAGATGAGGACT 780
QY 800 CACATCAACCCCTGTTGGGGAACAAAGGCTGACAGCTGTTGGGGCTCAAAATTTCCAGAA 859
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QY 860 GACCAACCATCCACTCAGCCCTCTGGGGTGTGTTGGGCTCTATATACCACTTCTGCTC 919
DB 841 GACCAACCATCCACTCAGCCCTCTGGGGTGTGTTGGGCTCTATATACCACTTCTGCTC 900
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QY 980 AGCTGCCCTGTCTCCAGAGAGACCGGAGTGTCTTACCTGTGTGACGCCCTTGGAACTTG 1039
DB 961 AGCTGCCCTGTCTCCAGAGAGACCGGAGTGTCTTACCTGTGTGACGCCCTTGGAACTTG 1020
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QY 1580 TCTGATTAATACAGACCTCTGTC 1600
DB 1561 TCTGATTAATACAGACCTCTGTC 1581

RESULT 4
US-10-033-301-15
; Sequence 15, Application US/10033301
; Patent No. 6930172
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman





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; PRIOR APPLICATION NUMBER: 60/089514  
; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089532  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
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Query Match 98.7%; Score 1579.4; DB 3; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 1 CAGCCACAGACGGGTATGAGCGGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCC 60  
  
Qy 80 ACTGCCAGGAGTCAGCGCGCTCTCTGCCAGTTTGGACAGATTTCAGCATGTGGAAGGT 139  
Db 61 ACTGCCAGGAGTCAGCGCGCTCTCTGCCAGTTTGGACAGATTTCAGCATGTGGAAGGT 120  
  
Qy 140 GTCCGACCTGCCCGGCAATGGACCCCTAAGAACACCCAGCTGCACAGCGCTTGGGGTG 199  
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Db 181 CCAGGACAGCTTGTATGCTCATTCAGAGCGGACCCCAAGTAGCTGTGTCTTCAAGGG 240  
  
Qy 260 CTGCACGGAGGCCAAGGACCCAGGAGCCCGCTCAGTGACACCGGATGGCCCGGCT 319  
Db 241 CTGCACGGAGGCCAAGGACCCAGGAGCCCGCTCAGTGACACCGGATGGCCCGGCT 300  
  
Qy 320 CTCCTCTGATCTCTACACCTTCTGTGTGCCCGCAGGAGGACTTCTGCAACACCTCGTTAA 379  
Db 301 CTCCTCTGATCTCTACACCTTCTGTGTGCCCGCAGGAGGACTTCTGCAACACCTCGTTAA 360  
  
Qy 380 CTCCTCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGTAGGTGCCCAGT 439  
Db 361 CTCCTCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGTAGGTGCCCAGT 420  
  
Qy 440 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGAGATCTGCCCCAGGGGAC 499  
Db 421 CTGCTTGTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGAGATCTGCCCCAGGGGAC 480  
  
Qy 500 CACACACTGTTATGATGGCTCTCTCAGGCTCAGGAGGAGGAGGATCTTCTCCAACTCTGAG 559  
Db 481 CACACACTGTTATGATGGCTCTCTCAGGCTCAGGAGGAGGAGGATCTTCTCCAACTCTGAG 540  
  
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Db 541 AGTCCAGGAGTGCATGCCCGCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTTGG 600  
  
Qy 620 GCCCGTGGGTATGACTGAGAACCTGCAATAGGAAGATTTTCTACCTGTCTATCGGGGAC 679  
Db 601 GCCCGTGGGTATGACTGAGAACCTGCAATAGGAAGATTTTCTACCTGTCTATCGGGGAC 660  
  
Qy 680 CACCATTTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACTCGAATAC 739  
Db 661 CACCATTTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACTCGAATAC 720  
  
Qy 740 CGAGATGTGCGAGGTGGGGCAGGTGTGTCTCAGGAGACGCTGCTCTCATAGATGTAGGACT 799  
Db 721 CGAGATGTGCGAGGTGGGGCAGGTGTGTCTCAGGAGACGCTGCTCTCATAGATGTAGGACT 780

QY 800 CACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAAATTCACAGAA 859  
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Db 781 CACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAAATTCACAGAA 840  
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QY 860 GACCACCATCCACTAGCCCTCTCTGGGGTGTCTTGGGCTCTCTATACCACACTTCGTCTC 919  
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Db 841 GACCACCATCCACTAGCCCTCTCTGGGGTGTCTTGGGCTCTCTATACCACACTTCGTCTC 900  
| | | | |  
QY 920 CTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTCCTGTAATCCCTCCCTCCTCA 979  
| | | | |  
Db 901 CTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTCCTGTAATCCCTCCCTCCTCA 960  
| | | | |  
QY 980 AGCTGCCCTGTCTCCAGGAGACCGGCGAGTGTCTACTCTGTGTCAGCCCTTTGGAACTGTG 1039  
| | | | |  
Db 961 AGCTGCCCTGTCTCCAGGAGACCGGCGAGTGTCTACTCTGTGTCAGCCCTTTGGAACTGTG 1020  
| | | | |  
QY 1040 TTCAAGTGGTCTCCCGCAATGACCTGTGCCCGGAGGCGGCACTCATTTGTTATGATGGTA 1099  
| | | | |  
Db 1021 TTCAAGTGGTCTCCCGCAATGACCTGTGCCCGGAGGCGGCACTCATTTGTTATGATGGTA 1080  
| | | | |  
QY 1100 CATTCACTCTCAGGAGTGGGCTGTCCACCAAAATGACATTTACAGGGCTGGTGGCCCA 1159  
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Db 1081 CATTCACTCTCAGGAGTGGGCTGTCCACCAAAATGACATTTACAGGGCTGGTGGCCCA 1140  
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QY 1160 ACCTTCAGCTTCTTGTGAAACACACACAGACAAATCGGGATCTTCTCTCGCGCTGAGAA 1219  
| | | | |  
Db 1141 ACCTTCAGCTTCTTGTGAAACACACACAGACAAATCGGGATCTTCTCTCGCGCTGAGAA 1200  
| | | | |  
QY 1220 GGTGATGTGAGCTCTCTGCTCTCAGCATGAGGAGTGGGCTGAGGGCTTGAGGTC 1279  
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## RESULT 6

US-09-992-598-354  
; Sequence 354, Application US/09992598  
; Patent No. 6956108  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.  
/ APPLICANT: Grimaldi, J. Christopher  
/ APPLICANT: Gurney, Austin L.  
/ APPLICANT: Kljavin, Ivar J.  
/ APPLICANT: Napier, Mary A.  
/ APPLICANT: Pan, James  
/ APPLICANT: Paoni, Nicholas F.  
/ APPLICANT: Roy, Margaret Ann  
/ APPLICANT: Stewart, Timothy A.  
/ APPLICANT: Tumas, Daniel  
/ APPLICANT: Watanabe, Colin K.  
/ APPLICANT: Williams, P. Mickey  
/ APPLICANT: Wood, William I.  
/ APPLICANT: Zhang, Zemin  
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
/ FILE REFERENCE: P2730PJC20  
/ CURRENT APPLICATION NUMBER: US/09/992,598  
/ CURRENT FILING DATE: 2001-11-14  
/ PRIOR APPLICATION NUMBER: 60/049787  
/ PRIOR FILING DATE: 1997-06-16  
/ PRIOR APPLICATION NUMBER: 60/062250  
/ PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579, 4; DB 3; Length 1587;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 15, Application US/10033435
; Patent No. 6969758
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2930R1C5
; CURRENT APPLICATION NUMBER: US/10/033,435
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/095,325
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/112,851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,145
; PRIOR FILING DATE: 1998-12-16
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119,341
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119,537
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; PRIOR FILING DATE: 1999-02-12
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; PRIOR APPLICATION NUMBER: 60/170,262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187,202
; PRIOR FILING DATE: 2000-03-03
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; PRIOR FILING DATE: 1999-06-02
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
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US-10-033-435-15

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Best Local Similarity 99.9%; Pred. No. 0;  
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; Sequence 354, Application US/09989735  
; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC61  
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CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-09

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RESULT 9

US-09-989-726-354

/ Sequence 354, Application US/09989726

/ Patent No. 7018811

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi J.

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Botstein, David

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Eaton, Dan L.

/ APPLICANT: Ferrara, Napoleone

/ APPLICANT: Fong, Sherman

/ APPLICANT: Gerber, Hanspeter

/ APPLICANT: Gerritsen, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Klijavin, Ivar J.

/ APPLICANT: Napier, Mary A.

/ APPLICANT: Pan, James

/ APPLICANT: Paoni, Nicholas F.

/ APPLICANT: Roy, Margaret Ann

/ APPLICANT: Stewart, Timothy A.

/ APPLICANT: Tumas, Daniel

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Williams, P. Mickey

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ TITLE OF INVENTION: Acids Encoding the Same

/ FILE REFERENCE: P2730PIC60

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/ CURRENT FILING DATE: 2001-11-19

/ PRIOR APPLICATION NUMBER: 60/049787

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RESULT 10  
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; Sequence 354, Application US/09997514  
; Patent No. 7019116  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC46  
; CURRENT APPLICATION NUMBER: US/09/997,514  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-02		Best Local Similarity		39.9%; Pred. No. 0;	
; PRIOR APPLICATION NUMBER: 60/091633		Matches 1580; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
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; PRIOR FILING DATE: 1998-07-09					
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## RESULT 11

US-09-989-728-354  
; Sequence 354, Application US/09989728  
; Patent No. 7029873  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC72  
; CURRENT APPLICATION NUMBER: US/09/989,728  
; PRIOR FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 5; Length 1587;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGCCACAGACGGGTTCATGAGCGCGGTATTACTGTGGCCCTCTCTGGGGTTCATCTCC 79

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QY 80 ACTGCCAGGAGTGACGGCGCTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGGAGGT 139

Db 61 ACTGCCAGGAGTGACGGCGCTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGGAGGT 120

QY 140 GTCCGACCTGCCCCCGGCAATGGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTG 199

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Db 181 CCAGGACAGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTTCCAGGG 240

QY 260 CTGCAGGAGGCCAAGGACAGAGCCCGCGTCACTGAGCACCGGATGGGCCCCCGCCT 319

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RESULT 12  
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; Sequence 354, Application US/09997349  
; Patent No. 7034106  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC37  
; CURRENT APPLICATION NUMBER: US/09/997,349  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
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40	PRIOR FILING DATE: 1998-07-02
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45	PRIOR APPLICATION NUMBER: 60/091626
46	PRIOR FILING DATE: 1998-07-02
47	PRIOR APPLICATION NUMBER: 60/091633
48	PRIOR FILING DATE: 1998-07-02
49	PRIOR APPLICATION NUMBER: 60/091978
50	PRIOR FILING DATE: 1998-07-07
51	PRIOR APPLICATION NUMBER: 60/091982
52	PRIOR FILING DATE: 1998-07-07
53	PRIOR APPLICATION NUMBER: 60/092182
54	PRIOR FILING DATE: 1998-07-09

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	Best Local Similarity	99.9%	Pred. No. 0						
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y	80	ACTGCCAGGAGTGCAGGCGGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAGGT							139
b	61	ACTGCCAGGAGTGCAGGCGGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAGGT							120
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Db 361 CTCCTCTCCGCTTTGGGCCCCACAGCCCGCCAGCAGACCCAGGATCTCTGAGGTGCCAGT 420  
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Db 481 CACACACTTGTATGAGTGGCTCTCAGGCTCAGGGAGGAGGACTTCTCCAATCTGAG 540  
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## RESULT 13

US-09-997-653-354

; Sequence 354, Application US/09997653

; Patent No. 7034122

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC38

; CURRENT APPLICATION NUMBER: US/09/997,653

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

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; PRIOR APPLICATION NUMBER: 60/066770

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; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

[illegible]



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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 98.7%; Score 1579.4; DB 5; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGCCACAGACGGGTGATGAGCGCGGTATTACTGTGCGCCCTCTCGGGTTCATCTCC 79  
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DB 661 CACCATATGACACAGGAACTTGGCTCAAGAACCCACTGATTTGACACACATCGAATAC 720  
QY 740 CGAGATGTGCGAGTGGGGCAGGTGTGTCTAGGAGACGCTGCTCTCATAGATAGGACT 799  
DB 721 CGAGATGTGCGAGTGGGGCAGGTGTGTCTAGGAGACGCTGCTCTCATAGATAGGACT 780  
QY 800 CACATCAACCTCGTGGGACAAAGGCTGCAGCCTCTGTTGGGCTCAAAATTCAGAA 859  
DB 781 CACATCAACCTCGTGGGACAAAGGCTGCAGCCTCTGTTGGGCTCAAAATTCAGAA 840  
QY 860 GACACACCTCACTCAGCCCTCTGCGGTGCTGTGGCTCTATACCACTTCGCTC 919  
DB 841 GACACACCTCACTCAGCCCTCTGCGGTGCTGTGGCTCTATACCACTTCGCTC 900

QY 920 CTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTTGTCTGAACCTCCCTCCCTCTCA 979  
DB 901 CTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTTGTCTGAACCTCCCTCCCTCTCA 960  
QY 980 AGCTGCCCTGTCTCCAGGAGACGGGAGTGTCTTACTGTGTGACGCCCCCTTGGAACTG 1039  
DB 961 AGCTGCCCTGTCTCCAGGAGACGGGAGTGTCTTACTGTGTGACGCCCCCTTGGAACTG 1020  
QY 1040 TTCAAGTGGCTCCCCCGAATGACCTGCCCGGAGGCGCACCTCATTTGTTATGATGGTA 1099  
DB 1021 TTCAAGTGGCTCCCCCGAATGACCTGCCCGGAGGCGCACCTCATTTGTTATGATGGTA 1080  
QY 1100 CATTCATCTCTCAGGAGTGGGCTGTCCACCAAAATGACATTCAGGGCTGCGTGCCCA 1159  
DB 1081 CATTCATCTCTCAGGAGTGGGCTGTCCACCAAAATGACATTCAGGGCTGCGTGCCCA 1140  
QY 1160 ACTTCCAGCTTCTTGTGAAACACACAGACAAATCGGGATCTTCTCTGCGGCTGAGAA 1219  
DB 1141 ACTTCCAGCTTCTTGTGAAACACACAGACAAATCGGGATCTTCTCTGCGGCTGAGAA 1200  
QY 1220 GGTGATGTGACAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTGAGGTC 1279  
DB 1201 GGTGATGTGACAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTGAGGTC 1260  
QY 1280 TCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTGTGGGGAGTGGTTTGGCCC 1339  
DB 1261 TCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTGTGGGGAGTGGTTTGGCCC 1320  
QY 1340 TTCTGCTTAACCTATTACCCCGACGATTTCTCAACCGCTGTGACACACCACTCAACC 1399  
DB 1321 TTCTGCTTAACCTATTACCCCGACGATTTCTCAACCGCTGTGACACCACTCAACC 1380  
QY 1400 TCCTCTGACCTATAACCTAATGGCTTGGACACCAAGATTTCTTCCCATTTCTGTCCATG 1459  
DB 1381 TCCTCTGACCTATAACCTAATGGCTTGGACACCAAGATTTCTTCCCATTTCTGTCCATG 1440  
QY 1460 AATCATTTTCCACACACAAATCATATCTATCTACCTAACACAGAACACTGGGGAGA 1519  
DB 1441 AATCATTTTCCACACACAAATCATATCTATCTACCTAACACAGAACACTGGGGAGA 1500  
QY 1520 GCTTGAGCATCGGACTTGGCTTGGAGAGGGGACCTTGGAGAGTGGCTGTCATGTA 1579  
DB 1501 GCTTGAGCATCGGACTTGGCTTGGAGAGGGGACCTTGGAGAGTGGCTGTCATGTA 1560  
QY 1580 TCTGATAATACAGCCCTGTC 1600  
DB 1561 TCTGATAATACAGCCCTGTC 1581

RESULT 14  
US-09-989-293A-354  
; Sequence 354, Application US/09989293A  
; Patent No. 7034136  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gromaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C66  
; CURRENT APPLICATION NUMBER: US/09/989,293A  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
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; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089512  
; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089514  
; PRIOR FILING DATE: 1998-06-16  
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; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089538  
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; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
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; PRIOR FILING DATE: 1998-06-18  
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; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090252  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090254  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090349  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: 60/090355  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: 60/090429  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090431  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090435  
; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090542  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090676



## RESULT 15

US-09-073-569-1  
; Sequence 1, Application US/09073569  
; Patent No. 6084088  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Grosmann, Angelika  
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,569  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 97-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1733 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 34...1344  
; OTHER INFORMATION:  
US-09-073-569-1

Query Match 98.4%; Score 1574.6; DB 3; Length 1733;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1577; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	20	CAGCCACAGAGCGGTTCATGAGCGCGGTATCTGCTGCGCCCTCTCTGCGGGTTTCATCTCC	79
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Qy	80	ACTGCCAGAGGTGAGCGCGGTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAAGGT	139
Db	78	ACTGCCAGAGGTGAGCGCGGTCTCTGCCAGTTTGGGACAGTTTCAGCTTGTGTGGAAGGT	137
Qy	140	GTCGGACCTCCCGGCAATGGACCCCTTAAGACACCACTGCGACAGCGGCTTGGGGTG	199
Db	138	GTCGGACCTCCCGGCAATGGACCCCTTAAGACACCACTGCGACAGCGGCTTGGGGTG	197
Qy	200	CCAGGACACGTTGATGTCTATTGAGAGCGGACCCCAAGTGAGCTGTGTCTCCAAGGG	259
Db	198	CCAGGACACGTTGATGTCTATTGAGAGCGGACCCCAAGTGAGCTGTGTCTCCAAGGG	257
Qy	260	CTGACCGGAGGCCAAGGACCAAGGAGCCCGCGTCACTGAGCAACCGGATGGGCCCGCCT	319
Db	258	CTGACCGGAGGCCAAGGACCAAGGAGCCCGCGTCACTGAGCAACCGGATGGGCCCGCCT	317

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380 CTCCCTCCCGTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGGGTGCCAGT 439  
378 CTCCCTCCCGTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGGGTGCCAGT 437  
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858 GACCACCATCACTCAGCCCTCTCTGGGGTCTTGTGGCTCTATACCCACTTCTGCTC 917  
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978 AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTACCTGTGTGAGCGGCTTGGACCTG 1037  
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1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCTGGGCCA 1159  
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1220 GCGTGATGTGAGCTCTCTGCTCTCAGCATGAGGAGGTGGGGCTCAGGGCTTGGAGTC 1279  
1218 GCGTGATGTGAGCTCTCTGCTCTCAGCATGAGGAGGTGGGGCTCAGGGCTTGGAGTC 1277  
1280 TCTCAGCTTGGGGGTGGGGCTGGCACTGGCCCCCAGCGCTGTGTGTGGGAGGTGTTGCC 1339  
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Db	1398		TCCCTCTGACCTCATAACTAATGGCTTGGACACAGATTCTTTCCCATTTCTGTCCATG	1457
Qy	1460		AATCATCTTCCCGACACACAATCAATCATATCTACTCAGCTAACAGCAACACTGGGGAGA	1519
Db	1458		AATCATCTTCCCGACACACAATCAATCATATCTATTACCTAACAGCAACACTGGGGAGA	1517
Qy	1520		GCCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1579
Db	1518		GCCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1577
Qy	1580		TCTGATAATACAGACCCCTGTC	1600
Db	1578		TCTGATAATACAGACCCCTGTC	1598

Search completed: July 11, 2006, 10:48:01  
 Job time : 327 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:35:03 ; Search time 8842 Seconds  
(without alignments)

11571.576 Million cell updates/sec

Title: US-10-727-619-1

Perfect score: 1600

Sequence: 1 aaagcagaagagattacc.....ctgataatacagaccctgtc 1600

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gE\_v.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_pa.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1600	100.0	1600	2	BD243146*
2	1600	100.0	1600	2	AR455749
3	1600	100.0	1600	2	AX107816
4	1599.6	100.0	1630	5	AF146747
5	1584	99.0	1597	5	HSA290452
6	1579.4	98.7	1587	2	CQ970596
7	1579.4	98.7	1587	2	AR252615
8	1579.4	98.7	1587	2	AR693505
9	1579.4	98.7	1587	2	AR706057
10	1579.4	98.7	1587	2	AR706205
11	1579.4	98.7	1587	2	AR757430
12	1579.4	98.7	1587	2	AR758930
13	1579.4	98.7	1587	2	AR773790
14	1579.4	98.7	1587	2	AR776244
15	1579.4	98.7	1587	2	AX358908
16	1579.4	98.7	1587	2	AX362401
17	1579.4	98.7	1587	2	AX403467
18	1579.4	98.7	1587	2	AX464332

19	1579.4	98.7	1587	5	AY358932	AY358932 Homo sapi
20	1576.6	98.5	1675	5	BC029167	BC029167 Homo sapi
21	1574.6	98.4	1733	2	BD062047	BD062047 Novel tum
22	1571.4	98.2	1613	2	BD222692	BD222692 Human sig
23	1440.6	90.0	1717	5	HSA310433	AJ310433 Homo sapi
24	1313	82.1	1314	5	BT020111	BT020111 Homo sapi
25	1313	82.1	1314	8	AY888472	AY888472 Synthetic
26	1312	82.0	1314	8	AY891246	AY891246 Synthetic
27	1312	82.0	1314	8	AY893778	AY893778 Synthetic
28	1193.2	74.6	1511	5	HSA305326	AB05326 Homo sapi
29	913	57.1	1311	2	BD062049	BD062049 Novel tum
30	492.8	30.8	243197	5	AC005392	AC005392 Homo sapi
31	464	29.0	2117	6	BC005615	BC005615 Mus muscu
32	464	29.0	2733	6	BC027283	BC027283 Mus muscu
33	436.6	27.3	450	2	AX969593	AX969593 Sequence
34	436.6	27.3	450	2	BD108312	BD108312 EST and e
35	436.6	27.3	450	2	AC412759	AC412759 Sequence
36	416	26.0	243197	5	AC005392	AC005392 Homo sapi
37	392.8	24.6	185409	5	AC018758	AC018758 Homo sapi
38	345.4	21.6	370	2	AR379742	AR379742 Sequence
39	187	11.7	469	2	CQ069683	CQ069683 Sequence
40	187	11.7	469	2	CQ068844	CQ068844 Sequence
41	187	11.7	469	2	CQ135644	CQ135644 Sequence
42	187	11.7	469	2	CQ174033	CQ174033 Sequence
43	187	11.7	469	2	CQ218940	CQ218940 Sequence
44	187	11.7	469	2	CQ257512	CQ257512 Sequence
45	187	11.7	469	2	CQ294747	CQ294747 Sequence

#### ALIGNMENTS

RESULT 1	BD243146	The gene PRV-1 and its use.	1600 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD243146					
DEFINITION	BD243146					
ACCESSION	BD243146					
VERSION	BD243146.1	GI:33052916				
KEYWORDS	JP 2002528077-A/1.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominidae; Homo.					
REFERENCE	1 (bases 1 to 1600)					
AUTHORS	Pahl,H.					
TITLE	The gene PRV-1 and its use					
JOURNAL	Patent: JP 2002528077-A 1 03-SEP-2002;					
	UNIVERSITAETSKLINIKUM FREIBURG					
COMMENT	OS Homo sapiens (human)					
	PN JP 2002528077-A/1					
	PD 03-SEP-2002					
	PF 30-SEP-1999 JP 2000578440					
	PR 23-OCT-1998 DE 198 49 044.5					
	PI HEIKE PAHL					
	PC C12N15/09 A61K31/7105, A61K31/711, A61K38/00, A61K39/395 PC					
	, A61K39/395, A61K48/00,					
	PC A61P7/00, A61P7/02, A61P7/06, A61P9/00, A61P9/12, A61P13/12 PC					
	, A61P17/04, A61P19/06,					
	PC A61P25/04, A61P29/00, A61P31/04, A61P35/00, A61P35/02, A61P43/00,					
	PC C07K14/47,					
	PC C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/ PC					
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VERSION AR455749.1 GI:42690638  
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SOURCE Unknown.  
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## REFERENCE

1 (bases 1 to 1600)  
Pohl, H.  
PRV-1 gene and the use thereof  
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VERSION AX107816.1 GI:13923217  
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REFERENCE 1  
AUTHORS Pahl, H.  
TITLE The prv-1 gene and use thereof  
JOURNAL Patent: WO 0123554-A 1 05-APR-2001;  
Universitaetsklinikum Freiburg (DE)  
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ACCESSION AJ290452  
VERSION AJ290452.1 GI:14970726  
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SOURCE Homo sapiens (human)  
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REFERENCE  
AUTHORS Kissel K., Santoso S., Hofmann C., Stroncek D. and Bux J.  
TITLE Molecular basis of the neutrophil glycoprotein NBI (CD177) involved in the pathogenesis of immune neutropenias and transfusion reactions  
JOURNAL Eur. J. Immunol. 31 (5), 1301-1309 (2001)  
PUBMED 11465086  
REFERENCE 2 (bases 1 to 1597)  
AUTHORS Kissel, K.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-2000) Kissel K., Justus-Liebig-University, Institute for Clinical Immunology and Transfusion Medicine, Langhansstrasse 7, 35385 Giessen, GERMANY

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QY	189	GGCTTGGGGTCCAGGACAGCTTGATGCTCAATTGAGACGGACCCCAAGTGAAGCTGGTG	248							
Db	181	GGCTTGGGGTCCAGGACAGCTTGATGCTCAATTGAGACGGACCCCAAGTGAAGCTGGTG	240							
QY	249	CTCTCAAGGGCTGCACGGAGGCCAAGGACAGGAGCCCGCGTCACTGAGCACCGGATG	308							
Db	241	CTCTCAAGGGCTGCACGGAGGCCAAGGACAGGAGCCCGCGTCACTGAGCACCGGATG	300							
QY	309	GGCCCCGGCTCTCCCTGATCTCTTACACCTTGTGTGGCCCAAGGAGGACTTCTTGCAC	368							
Db	301	GGCCCCGGCTCTCCCTGATCTCTTACACCTTGTGTGGCCCAAGGAGGACTTCTTGCAC	360							
QY	369	AACCTGTTAACTCCCTCCCGCTTTGGGCCCAACAGCCCCCAGCAGACCCAGGATCTCTG	428							
Db	361	AACCTGTTAACTCCCTCCCGCTTTGGGCCCAACAGCCCCCAGCAGACCCAGGATCTCTG	420							
QY	429	AGGTGCCCGCTCTCTTGTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGATCTGCG	488							
Db	421	AGGTGCCCGCTCTCTTGTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGATCTGCG	480							

Qy	489	CCCAAGGGACCAACACATGTTTATGATGGCTCTCTCAGGCTCAGGGAGGAGGATCTTC	548
Db	481	CCCAAGGGACCAACACATGTTTATGATGGCTCTCTCAGGCTCAGGGAGGAGGATCTTC	540
Qy	549	TCCAATCTGAGAGTCCAGGATGTCATGCCACGACGAGTTGCAACCTGCTCAATGGGACA	608
Db	541	TCCAATCTGAGAGTCCAGGATGTCATGCCACGACGAGTTGCAACCTGCTCAATGGGACA	600
Qy	609	CAGGAAATTTGGGCCCTGGGTATGACTGAGAACTGCAATAGGAAAGATTTCTGACCTGT	668
Db	601	CAGGAAATTTGGGCCCTGGGTATGACTGAGAACTGCAATAGGAAAGATTTCTGACCTGT	660
Qy	669	CATCGGGGACCAACCAATTAATGACACACGAAACTTGGCTCAAGAACCCACTGATGGACC	728
Db	661	CATCGGGGACCAACCAATTAATGACACACGAAACTTGGCTCAAGAACCCACTGATGGACC	720
Qy	729	ACATCGAATACCGAGATGTCGAGGTGGGACAGGTGTGTCAGGAGACGCTGCTCATATA	788
Db	721	ACATCGAATACCGAGATGTCGAGGTGGGACAGGTGTGTCAGGAGACGCTGCTCATATA	780
Qy	789	GATGTAGGACTCACATCAACCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAA	848
Db	781	GATGTAGGACTCACATCAACCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAA	840
Qy	849	AATTCCAGAGAACCAACCATCCACTCAGCCCCCTCTGGGGTGTGTTGGGCTCTCTATACC	908
Db	841	AATTCCAGAGAACCAACCATCCACTCAGCCCCCTCTGGGGTGTGTTGGGCTCTCTATACC	900
Qy	909	CACCTTCTGCTCCGACCTGTGCAATAGTGCAGACGACGAGCGCTTCTGCTGAATCC	968
Db	901	CACCTTCTGCTCCGACCTGTGCAATAGTGCAGACGACGAGCGCTTCTGCTGAATCC	960
Qy	969	CTCCCTCTCAAGCTGCCCTGTCCAGGAGACCGGCACTGTCTACTCTGTGTGAGGCC	1028
Db	961	CTCCCTCTCAAGCTGCCCTGTCCAGGAGACCGGCACTGTCTACTCTGTGTGAGGCC	1020
Qy	1029	CTTGGAACTGTTCAAAGTGGCTCCCCCGAATGACTGTGCCCGGAGGCGGCACCTATGT	1088
Db	1021	CTTGGAACTGTTCAAAGTGGCTCCCCCGAATGACTGTGCCCGGAGGCGGCACCTATGT	1080
Qy	1089	TATGATGGGTACATTCATCTCAGGAGTGGGCTGCCACCAAAATGAGCATTCAGGGC	1148
Db	1081	TATGATGGGTACATTCATCTCAGGAGTGGGCTGCCACCAAAATGAGCATTCAGGGC	1140
Qy	1149	TGCGTGGCCCAAACCTTTCAGCTTCTTGTGTAACCAACCAACAGAAATCGGGATCTTCTCT	1208
Db	1141	TGCGTGGCCCAAACCTTTCAGCTTCTTGTGTAACCAACAGAAATCGGGATCTTCTCT	1200
Qy	1209	GCSCGTGAGAGCGTGAATGTCAGCTCTCTGCTCTCAGATGAGGAGGTGGGGCTGAG	1268
Db	1201	GCSCGTGAGAGCGTGAATGTCAGCTCTCTGCTCTCAGATGAGGAGGTGGGGCTGAG	1260
Qy	1269	GGCTTGGAGTCTCTCACTTGGGGGTGGGCTGSCACTGGCCCCCAGCGCTGTGTGGGGA	1328
Db	1261	GGCTTGGAGTCTCTCACTTGGGGGTGGGCTGSCACTGGCCCCCAGCGCTGTGTGGGGA	1320
Qy	1329	GTGCTTGGCCCTCTCTGCTAACTTATTAACCCCAACGATTCCTTCCCGCTGCTGACACC	1388
Db	1321	GTGCTTGGCCCTCTCTGCTAACTTATTAACCCCAACGATTCCTTCCCGCTGCTGACACC	1380
Qy	1389	CACACTCAAACCTCCCTCTGACCTCAATTAACCTAATATGAGGCTTGGACACAGGATCTTCCCA	1448
Db	1381	CACACTCAAACCTCCCTCTGACCTCAATTAACCTAATATGAGGCTTGGACACAGGATCTTCCCA	1440
Qy	1449	TTCTGTTCATGAATCATCTTCCACACACAACTAATATGAGGCTTGGACACAGGATCTTCCCA	1508
Db	1441	TTCTGTTCATGAATCATCTTCCACACACAACTAATATGAGGCTTGGACACAGGATCTTCCCA	1500
Qy	1509	CACCTGGGAGAGCGCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGGACGCTGGAGGAGT	1568
Db	1501	CACCTGGGAGAGCGCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGGACGCTGGAGGAGT	1560

Qy 1569 GGCTGCATGTATCTGATAATACAGACCCTGTC 1600  
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RESULT 6  
CQ970596  
LOCUS CQ970596 1587 bp DNA linear PAT 05-JAN-2005  
DEFINITION Sequence 161 from Patent EP1489095.  
ACCESSION CQ970596  
VERSION CQ970596.1 GI:57162779  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Polypeptide, nucleic acid encoding it, and their use for the  
diagnosis of cancer  
JOURNAL Patent: EP-1489095-A 161 22-DEC-2004;  
Genentech Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..1587  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 98.7%; Score 1579.4; DB 2; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CAGCCACAGAGCGGTGCTGAGCGCGGTATTACTGTCGCCCTCTCGGGGTTTCATCCTCCC 79  
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Qy 80 ACTGCCAGAGTGAGCGGTGCTGCTGCGAGTTGGGACAGTTGAGCATGTTGGAAGGT 139  
Db 61 ACTGCCAGAGTGAGCGGTGCTGCTGCGAGTTGGGACAGTTGAGCATGTTGGAAGGT 120

Qy 140 GTCCGACTGCCCCGGAATGGACCCCTTAGAACACAGCTGCGACAGCGGCTTGGGGTG 199  
Db 121 GTCCGACTACCCCGGAATGGACCCCTTAGAACACAGCTGCGACAGCGGCTTGGGGTG 180

Qy 200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGGCTGCTCTCAAGGG 259  
Db 181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGGCTGCTCTCAAGGG 240

Qy 260 CTGACCGGAGCCCAAGGACCAAGGACCCCGGTCACTGAGCACCGGATGGGCCCGGCGCT 319  
Db 241 CTGACCGGAGCCCAAGGACCAAGGACCCCGGTCACTGAGCACCGGATGGGCCCGGCGCT 300

Qy 320 CTCCTCATCTCTACACCTTCGTGCGCCAGAGGACTTCTGCAACACACTCTGTTAA 379  
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Qy 380 CTCCTCTCCGCTTTGGGCCCCACAGCCCCAGCAGACCCAGGATCTTTGAGGTGCCAGT 439  
Db 361 CTCCTCTCCGCTTTGGGCCCCACAGCCCCAGCAGACCCAGGATCTTTGAGGTGCCAGT 420

Qy 440 CTGCTTGTATGAAGGCTGTCTGGAGGGGCAACAGAGAGATCTGCCCAAGGGGAC 499  
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Qy 500 CACACACTGTTATGATGCCCTCTCAGGCTCAGGGGAGGGGATCTTCTCAATCTGAG 559  
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Qy 560 AGTCCAGGATGTCATGCCCCAGCGGTTGCAACTGCTCAATGGGACACAGGAAATTGG 619

RESULT 7

Db 541 AGTCCAGGATGTCATGCCCCAGCCAGGTTGCAACTGCTCAATGGGACACAGGAAATTGG 600  
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Db 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTCTGACCTGTCTATCGGGGAC 660

Qy 680 CACCATTTATGACACACCGGAACTTGGCTCAAGAAACCCACTGATTGGACACATCGAATAC 739  
Db 661 CACCATTTATGACACACCGGAACTTGGCTCANGAACCCACTGATTGGACACATCGAATAC 720

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Qy 800 CACATCAACCTGTGTGGGGCAAAAGGCTGACGACACTGTTGGGCTCAAAATTCGCCAGAA 859  
Db 781 CACATCAACCTGTGTGGGGCAAAAGGCTGACGACACTGTTGGGCTCAAAATTCGCCAGAA 840

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Db 841 GACCACCATCCACTCAGCCCCCTCTGGGGTCTTGTGGCTCTCTATACCCACTTCTGCTC 900

Qy 920 CTCGGACCTGTGCAATAGTCCAGCAGCAGCGTTCTGTCTGAATCCCTCCCTCTCTCA 979  
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Qy 980 AGCTGCCCCCTGTCTCCAGGAGACCGGACGTGCTTACCTGTGTGAGCCCCCTTGGNACTG 1039  
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Qy 1040 TTCAAGTGGCTTCCCGCCGAATGACTGCTCCAGGGGCGCCACTCATTTGTTATGATGGTA 1099  
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Qy 1100 CATTCATCTCTCAGGAGGTGGGTGTCCACCAAAATGAGCAATTCAGGCTCGCTGGCCCA 1159  
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Qy 1280 TCTCAGCTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGTGGGAGTGGTTTGCC 1339  
Db 1261 TCTCAGCTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGTGGGAGTGGTTTGCC 1320

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Qy 1580 TCTGATAATACAGACCCCTGTC 1600  
Db 1561 TCTGATAATACAGACCCCTGTC 1581

AR252615  
LOCUS AR252615 1587 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 354 from patent US 6478825.  
ACCESSION AR252615  
VERSION AR252615.1 GI:27300523  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1587)  
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.  
TITLE Implant, method of making same and use of the implant for the  
treatment of bone defects  
JOURNAL Patent: US 6478825-A 354 12-NOV-2002;  
Osteotech, Inc.; Eatontown, NJ  
FEATURES  
source Location/Qualifiers  
1..1587  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 98.7%; Score 1579.4; DB 2; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 20 CAGCCACAGACGGGTGTCATGACGCGGTATTAATGCTGGCCCTCTCTGGGGTTTCATCTCC 79  
DB 1 CAGCCACAGACGGGTGTCATGACGCGGTATTAATGCTGGCCCTCTCTGGGGTTTCATCTCC 60  
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QY 200 CCAGGACACCTGTGATGCTCAATGAGAGCGGACCCCAAGTGGAGTGGTGGTGGGTTG 259  
DB 181 CCAGGACACCTGTGATGCTCAATGAGAGCGGACCCCAAGTGGAGTGGTGGGTTG 240  
QY 260 CTGACGGAGGCAAGGACCCAGGAGCCCGGTCCTGAGACCCGAGTGGGCGCCGCT 319  
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QY 560 AGTCCAGGGATGATGCCCCCAGGAGGTTGCAACTCTGCTCAATGGGACACAGGAAATTTGG 619  
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DB 1561 TCTGATAATAACAGACCCCTGTC 1581

RESULT 8  
LOCUS AR693505 1587 bp DNA linear PAT 14-SEP-2005  
DEFINITION Sequence 354 from patent US 6913919.  
ACCESSION AR693505  
VERSION AR693505.1 GI:75183962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1587)  
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and



Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: US 6913919-A 354 05-JUL-2005;  
Genetech, Inc.; South San Francisco, CA  
FEATURES Location/Qualifiers  
source 1..1587  
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Query Match										
Best Local Similarity 98.7%; Score 1579.4; DB 2; Length 1587;										
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;										
Qy	20	CAGCCACAGACGGGT	CATGAGCGGGT	ATTACTGCTGGCCCT	CTCTGGGGTT	CATCTCTCC	79			
Db	1	CAGCCACAGACGGGT	CAATGAGCGGGT	ATTACTGCTGGCCCT	CTCTGGGGTT	CATCTCTCC	60			
Qy	80	ACTGCCAGGAGT	GCAGGCGT	CTCTGCGAGTTT	GGGACAGTTT	CAGCATGTGT	GAAAGT	139		
Db	61	ACTGCCAGGAGT	GCAGGCGT	CTCTGCGAGTTT	GGGACAGTTT	CAGCATGTGT	GAAAGT	120		
Qy	140	GTCCGACCT	GTCCCGCAAT	GGACCCCTTA	AGAACACACAGCT	TCGACAGCGG	CTTGGGGTG	199		
Db	121	GTCCGACCT	ATCCCGCAAT	GGACCCCTTA	AGAACACACAGCT	TCGACAGCGG	CTTGGGGTG	180		
Qy	200	CGAGGACA	CGTTGAT	GTCTCATTTAGAG	CGGACCCCAAGTAGAGCT	TGTGCTCTCAA	GGG	259		
Db	181	CGAGGACA	CGTTGAT	GTCTCATTTAGAG	CGGACCCCAAGTAGAGCT	TGTGCTCTCAA	GGG	240		
Qy	260	CTGCACGGAGCC	CAAGGAC	CAGGAGCCCGCGT	CTACTAGACACCGGAT	TGGGCCCCGGCT	319			
Db	241	CTGCACGGAGCC	CAAGGAC	CAGGAGCCCGCGT	CTACTAGACACCGGAT	TGGGCCCCGGCT	300			
Qy	320	CTCCCTGAT	CTCTACACCTT	CTGTGTGCGCGCAGGAGAC	TTCCTGCAACAACCT	CGTTAA	379			
Db	301	CTCCCTGAT	CTCTACACCTT	CTGTGTGCGCGCAGGAGAC	TTCCTGCAACAACCT	CGTTAA	360			
Qy	380	CTCCCTCCCGT	TTTGGGCCCCACAGCCCC	CCAGCAGCACCGAT	CTCTTGGAGTG	CCCACT	439			
Db	361	CTCCCTCCCGT	TTTGGGCCCCACAGCCCC	CCAGCAGCACCGAT	CTCTTGGAGTG	CCCACT	420			
Qy	440	CTGCTTGT	CTATGGAAGG	CTGTCTGAGGGG	GAACAACAGAGAT	CTGCCCCAAGGGAC	499			
Db	421	CTGCTTGT	CTATGGAAGG	CTGTCTGAGGGG	GAACAACAGAGAT	CTGCCCCAAGGGAC	480			
Qy	500	CACACACT	GTATGAT	GGCTCTCTCAGGCT	CAGGGGAGG	GCATCTTCTCCAACT	CTGAG	559		
Db	481	CACACACT	GTATGAT	GGCTCTCTCAGGCT	CAGGGGAGG	GCATCTTCTCCAACT	CTGAG	540		
Qy	560	AGTCCAGGAT	GCATG	CCCCCAGCCAGG	TGCAACCTGCTCAAT	TGGGACACAGAAAT	TGG	619		
Db	541	AGTCCAGGAT	GCATG	CCCCCAGCCAGG	TGCAACCTGCTCAAT	TGGGACACAGAAAT	TGG	600		
Qy	620	GCCCGTGGGTA	TGACTGAGAACT	GCAAATAGGAAAGAT	TTTCTGACTCTG	TCATCGGGGAC	679			
Db	601	GCCCGTGGGTA	TGACTGAGAACT	GCAAATAGGAAAGAT	TTTCTGACTCTG	TCATCGGGGAC	660			
Qy	680	CACCAATTAT	GACACACGGAA	ACTTGGCTCA	AGAACCCCACTGAT	TGGGACACATCGAAT	TAC	739		
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Qy	740	CGAGAT	GTGCGAGT	TGGGCGAGGT	GTGTGAGGAC	GCCTGCTCATAGAT	GTAGGACT	799		
Db	721	CGAGAT	GTGCGAGT	TGGGCGAGGT	GTGTGAGGAC	GCCTGCTCATAGAT	GTAGGACT	780		
Qy	800	CACATCAACCT	TGTTGGGGA	CAAAAGG	TGCAGCACT	TGTGGGGT	CTAAAAAT	CCACGAA	859	
Db	781	CACATCAACCT	TGTTGGGGA	CAAAAGG	CTGAGCACT	TGTGGGGT	CTAAAAAT	CCACGAA	840	
Qy	860	GACCACCAT	CCACTCAG	CCCCCTCTCTGGGGT	GCTTGTGGCCCT	CTATACCCACT	CTCTGCTC	919		



Query Match		98.7%;	Score 1579.4;	DB 2;	Length 1587;	
Best Local Similarity		99.9%;	Pred. No. 0;			
Matches 1580;		Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
Qy	20	CAGCCACAGACGGGTATGAGCGCGGTATTA	CTGCTGGCCCTCTCTGGGGTTCATCTCTCC	79		
Db	1	CAGCCACAGACGGGTATGAGCGCGGTATTA	CTGCTGGCCCTCTCTGGGGTTCATCTCTCC	60		
Qy	80	ACTGCCAGGAGTGCAGGCGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAGGT	139			
Db	61	ACTGCCAGGAGTGCAGGCGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAGGT	120			
Qy	140	GTCGACCTGCCCGGCAATGGAACCCCTAAGAACACCCAGCTGCGACAGCGGCTTGGGGT	199			
Db	121	GTCGACCTGCCCGGCAATGGAACCCCTAAGAACACCCAGCTGCGACAGCGGCTTGGGGT	180			
Qy	200	CGAGGACAGTTGATGCTCATTTGAGAGCGGACCCCAAGTAGGCTGTGCTCCCAAGG	259			
Db	181	CCAGGACAGTTGATGCTCATTTGAGAGCGGACCCCAAGTAGGCTGTGCTCCCAAGG	240			
Qy	260	CTGCACGGAGCCCAAGGACGAGGCCCCCGCTCACTGAGCACCGGATGGGCCCCCGCCT	319			
Db	241	CTGCACGGAGCCCAAGGACGAGGCCCCCGCTCACTGAGCACCGGATGGGCCCCCGCCT	300			
Qy	320	CTCCCTGATCTCTACACCTTCTGTGTGCCGCCAGGAGGACTTCTGCACCAACCTCGTTAA	379			
Db	301	CTCCCTGATCTCTACACCTTCTGTGTGCCGCCAGGAGGACTTCTGCACCAACCTCGTTAA	360			
Qy	380	CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGACAGCCAGGATCTTTGAGGTGCCAGT	439			
Db	361	CTCCCTCCCGCTTTGGGCCCCCAGAGCCCCCAGAGACCCCAAGTAGGCTGTGCTCCCAAGG	420			
Qy	440	CTGCTTGTCTATGGAAGGCTGTCTGGAAGGGACAAACAGAAAGAGATCTGCCCCCAAGGGAC	499			
Db	421	CTGCTTGTCTATGGAAGGCTGTCTGGAAGGGACAAACAGAAAGAGATCTGCCCCCAAGGGAC	480			
Qy	500	CACACACTGTTATGATGGCCCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCAATCTGAG	559			
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Qy	560	AGTCCAGGATGATGCCCCAGCCAGGTTCGAACCTGCTCAATGGGACACAGGAATGG	619			
Db	541	AGTCCAGGATGATGCCCCAGCCAGGTTCGAACCTGCTCAATGGGACACAGGAATGG	600			
Qy	620	GCCCGTGGGTATGACTCAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC	679			
Db	601	GCCCGTGGGTATGACTCAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC	660			
Qy	680	CACCATTTATGACACACGGAACCTTGGCTCAAGAACCCACTGATTTGGACCACTCGAATAC	739			
Db	661	CACCATTTATGACACACGGAACCTTGGCTCAAGAACCCACTGATTTGGACCACTCGAATAC	720			
Qy	740	CGAGATGTGGAGTGGGGAGGTGTCTCAGGAGACGCTGCTGCTCATAGATGTAGACT	799			
Db	721	CGAGATGTGGAGTGGGGAGGTGTCTCAGGAGACGCTGCTGCTCATAGATGTAGACT	780			
Qy	800	CACATCAACCTGTGTGGGGACAAAGGCTGCAGCACTGTGTGGGCTCAAAATTTCCAGAA	859			
Db	781	CACATCAACCTGTGTGGGGACAAAGGCTGCAGCACTGTGTGGGCTCAAAATTTCCAGAA	840			
Qy	860	GACCACCATCACTCAGCCCCCTCTGGGGTGTCTGAGGCTCTCTATACCCACTTCTGCTC	919			
Db	841	GACCACCATCACTCAGCCCCCTCTGGGGTGTCTGAGGCTCTCTATACCCACTTCTGCTC	900			
Qy	920	CTGGACCTGTGCATAGTGGCAGCAGCAGGAGGTCTGCTGACCTCTCTCTCTCTCA	979			
Db	901	CTGGACCTGTGCATAGTGGCAGCAGCAGGAGGTCTGCTGACCTCTCTCTCTCTCA	960			
Qy	980	AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTACCTGTGTGAGGCCCTTGGAACTTG	1039			
Db	961	AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTACCTGTGTGAGGCCCTTGGAACTTG	1020			
Qy	1040	TTCAAGTGGCTCTCCCCCGGAATGACCTCGCCCGAGGGGCGCCACTCATTTGTTATGATGGGTA	1099			

Db	1021	TTCAAGTGGCTCTCCCCCGGAATGACCTGCCCCAGGGCGCCACTCATTTGTTATGATGGGTA	1080			
Qy	1100	CATTCACTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGCTGCGTGGGCCCA	1159			
Db	1081	CATTCACTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGCTGCGTGGGCCCA	1140			
Qy	1160	ACCTTCACAGTCTTCTTGAACCAACACACAGCAAAATCGGGATCTTCTCTCGCGTGAAG	1219			
Db	1141	ACCTTCACAGTCTTCTTGAACCAACACACAGCAAAATCGGGATCTTCTCTCGCGTGAAG	1200			
Qy	1220	GCGTATGTGCAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTCAGGGCTTGGAGTC	1279			
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Qy	1280	TCCTACTTGGGGGTGGGCTGGCACTGGCCCCCAGCGCTGTGTGGGGAGTGGTTTGGCC	1339			
Db	1261	TCCTACTTGGGGGTGGGCTGGCACTGGCCCCCAGCGCTGTGTGGGGAGTGGTTTGGCC	1320			
Qy	1340	TTCTCTTAACCTCTATTACCCCAACGATTTCTTCAACCGCTCTGACCAACCACTCAACC	1399			
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Qy	1400	TCCTCTGACCTCATTAACCTTAATGGCTTGGACACCAAGATTTCTTCCCATTTCTTCCATG	1459			
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Qy	1460	AATCATTTTCCCAACACAAATCATTCATCTACTTCACTTCACTTCACTTCACTTCACTTCACT	1519			
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Qy	1520	GCCTGGAGCATCGGACTTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1579			
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LOCUS		Sequence 15 from patent US 6930172.				
DEFINITION		AR706205				
ACCESSION		AR706205				
VERSION		AR706205.1	GI:75925073			
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unclassified.				
REFERENCE		1 (bases 1 to 1587)				
AUTHORS		Ferrara, N., Gao, W.-Q., Goddard, A., Gurney, A.L., Watanabe, C.K. and Wood, W.I.				
TITLE		Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL		Patent: US 6930172-A 15 16-AUG-2005;				
FEATURES		Genentech, Inc.; South San Francisco, CA				
source		Location/Qualifiers				
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Query Match		98.7%;	Score 1579.4;	DB 2;	Length 1587;	
Best Local Similarity		99.9%;	Pred. No. 0;			
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Qy	80	ACTGCCAGGAGTGCAGGCGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAGGT	139			
Db	61	ACTGCCAGGAGTGCAGGCGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAGGT	120			
Qy	140	GTCGACCTGCCCGGCAATGGAACCCCTAAGAACACCCAGCTGCGACAGCGGCTTGGGGT	199			
Db	121	GTCGACCTGCCCGGCAATGGAACCCCTAAGAACACCCAGCTGCGACAGCGGCTTGGGGT	180			
Qy	200	CGAGGACAGTTGATGCTCATTTGAGAGCGGACCCCAAGTAGGCTGTGCTCCCAAGG	259			
Db	181	CCAGGACAGTTGATGCTCATTTGAGAGCGGACCCCAAGTAGGCTGTGCTCCCAAGG	240			
Qy	260	CTGCACGGAGCCCAAGGACGAGGCCCCCGCTCACTGAGCACCGGATGGGCCCCCGCCT	319			
Db	241	CTGCACGGAGCCCAAGGACGAGGCCCCCGCTCACTGAGCACCGGATGGGCCCCCGCCT	300			
Qy	320	CTCCCTGATCTCTACACCTTCTGTGTGCCGCCAGGAGGACTTCTGCACCAACCTCGTTAA	379			
Db	301	CTCCCTGATCTCTACACCTTCTGTGTGCCGCCAGGAGGACTTCTGCACCAACCTCGTTAA	360			
Qy	380	CTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGACAGCCAGGATCTTTGAGGTGCCAGT	439			
Db	361	CTCCCTCCCGCTTTGGGCCCCCAGAGCCCCCAGAGACCCCAAGTAGGCTGTGCTCCCAAGG	420			
Qy	440	CTGCTTGTCTATGGAAGGCTGTCTGGAAGGGACAAACAGAAAGAGATCTGCCCCCAAGGGAC	499			
Db	421	CTGCTTGTCTATGGAAGGCTGTCTGGAAGGGACAAACAGAAAGAGATCTGCCCCCAAGGGAC	480			
Qy	500	CACACACTGTTATGATGGCCCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCAATCTGAG	559			
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Qy	560	AGTCCAGGATGATGCCCCAGCCAGGTTCGAACCTGCTCAATGGGACACAGGAATGG	619			
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Qy	620	GCCCGTGGGTATGACTCAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC	679			
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Qy	680	CACCATTTATGACACACGGAACCTTGGCTCAAGAACCCACTGATTTGGACCACTCGAATAC	739			
Db	661	CACCATTTATGACACACGGAACCTTGGCTCAAGAACCCACTGATTTGGACCACTCGAATAC	720			
Qy	740	CGAGATGTGGAGTGGGGAGGTGTCTCAGGAGACGCTGCTGCTCATAGATGTAGACT	799			
Db	721	CGAGATGTGGAGTGGGGAGGTGTCTCAGGAGACGCTGCTGCTCATAGATGTAGACT	780			
Qy	800	CACATCAACCTGTGTGGGGACAAAGGCTGCAGCACTGTGTGGGCTCAAAATTTCCAGAA	859			
Db	781	CACATCAACCTGTGTGGGGACAAAGGCTGCAGCACTGTGTGGGCTCAAAATTTCCAGAA	840			
Qy	860	GACCACCATCACTCAGCCCCCTCTGGGGTGTCTGAGGCTCTCTATACCCACTTCTGCTC	919			
Db	841	GACCACCATCACTCAGCCCCCTCTGGGGTGTCTGAGGCTCTCTATACCCACTTCTGCTC	900			
Qy	920	CTGGACCTGTGCATAGTGGCAGCAGCAGGAGGTCTGCTGACCTCTCTCTCTCTCA	979			
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Qy	980	AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTACCTGTGTGAGGCCCTTGGAACTTG	1039			
Db	961	AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTACCTGTGTGAGGCCCTTGGAACTTG	1020			
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Qy 1040 TTCAAGTGGCTTCCCCCGGAATGACTGCCCCAGGGGCGCACTCATTTGTTATGATGGGTA 1099  
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## RESULT 11

AR757430 LOCUS AR757430 1587 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 354 from patent US 6953836.  
ACCESSION AR757430  
VERSION AR757430.1 GI:83322601  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1587)  
AUTHORS Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.  
TITLE PRO844 polypeptides  
JOURNAL Patent: US 6953836-A 354 11-OCT-2005;  
Genentech, Inc.; South San Francisco, CA  
FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 98.7%; Score 1579.4; DB 2; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGACAGTTCAGCATGTGTGGAAGGT 120  
Qy 140 GTCGACCTGCCCGCAATGAGACCCCTAAGAACACAGCTGCGACAGCGCTTGGGGTG 199  
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RESULT 12  
AR758930  
LOCUS 1587 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 354 from patent US 6956108.  
ACCESSION AR758930  
VERSION AR758930.1 GI:83325025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1587)  
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.  
TITLE PRO184 antibodies  
JOURNAL Patent: US 6956108-A 354 18-OCT-2005;  
Genentech, Inc.; South San Francisco, CA;  
WOX;

FEATURES  
source Location/Qualifiers  
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Query Match 98.7%; Score 1579.4; DB 2; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
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DEFINITION Sequence 15 from patent US 6969758.  
ACCESSION AR773790  
VERSION AR773790.1 GI:83350971  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1587)  
AUTHORS Ferrara,N., Gao,W.-Q., Goddard,A., Gurney,A.L., Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: US 6969758-A 15 29-NOV-2005;  
Genentech, Inc.; South San Francisco, CA  
FEATURES  
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Db 1561 TCTGATAATACAGACCTGTG 1581

## RESULT 15

AX358908

LOCUS

DEFINITION Sequence 161 from Patent WO0193983.

ACCESSION AX358908

VERSION AX358908.1 GI:18675355

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

## REFERENCE

AUTHORS

Baker, K.P., Desnovers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

TITLE Watanabe, C.K. and Wood, W.I.  
JOURNAL Secreted and transmembrane polypeptides and nucleic acids encoding the same  
Patent: WO 0193983-A 161 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 98.7%; Score 1579.4; DB 2; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Job time : 8849 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:25:06 ; Search time 41 Seconds  
(without alignments)  
1025.530 Million cell updates/sec

Title: US-10-727-619-2

Perfect score: 2381

Sequence: 1 MSALLLLALLGFIPLPGVQ.....WGVLALPALWGWGVCPC 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_90.\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	163	6.8	5376	2 T42215	zonadhesin - mouse
2	143	6.0	1297	2 T30274	proteoliasin - se
3	142	6.0	330	1 JN0561	urokinase-type pla
4	136.5	5.7	1101	2 T16840	hypothetical prote
5	136.5	5.7	2531	2 A46019	notch-1 protein -
6	131.5	5.5	2813	1 VWHU	von Willebrand fac
7	130	5.5	2946	2 T15840	hypothetical prote
8	128	5.4	1408	2 S16148	gene serrate prote
9	127.5	5.4	1895	2 T15881	hypothetical prote
10	126.5	5.3	2090	2 T30075	hypothetical prote
11	126.5	5.3	2153	2 T30074	hypothetical prote
12	122.5	5.1	677	2 C42125	trophozoite cystei
13	122.5	5.1	1964	2 T09059	notch4 - mouse
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15	121.5	5.1	739	2 B88553	protein K04H4.2b [
16	121.5	5.1	2318	2 S45306	notch 3 protein -
17	119.5	5.0	327	2 A55356	urokinase-type pla
18	119.5	5.0	1357	2 T16860	hypothetical prote
19	118.5	5.0	1043	2 T19734	hypothetical prote
20	118.5	5.0	3020	2 A43932	mucin 2 precursor,
21	118	5.0	2703	1 A24420	notch protein - fr
22	117.5	4.9	1251	2 A57293	latent transformin
23	117	4.9	2395	1 S50820	surface protein ty
24	117	4.9	3002	2 A47221	fibrillin 1 precur
25	116	4.9	802	2 T42293	hypothetical prote
26	116	4.9	949	2 T24294	hypothetical prote
27	116	4.9	2704	2 S09118	G surface protein
28	115	4.8	667	2 A48579	trophozoite surfac
29	115	4.8	1743	2 T26859	hypothetical prote

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38	113.5	4.8	1797	2 T21889	hypothetical prote
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41	113	4.7	2195	2 T34264	hypothetical prote
42	113	4.7	2718	2 A23475	G surface protein
43	112	4.7	385	2 S53718	homeotic protein d
44	112	4.7	589	2 C38128	epithelin/granulin
45	112	4.7	2910	2 T42214	otogelin - mouse

ALIGNMENTS

RESULT 1

T42215

zonadhesin - mouse

N:Alternate names: sperm-specific membrane protein

C:Species: Mus musculus (house mouse)

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T42215

R:GAO, Z.; Garbers, D.L.

J. Biol. Chem. 273, 3415-3421, 1998

A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane p

A:Reference number: 222080; MUID:98123114; PMID:9452463

A:Accession: T42215

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-5376 <GAO>

A:Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:G3327420;

C:Genetics:

A:Gene: Zan

A:Map position: 5

C:Function:

A:Description: functions in multiple cell adhesion processes

A>Note: found exclusively on the apical region of the sperm head

C:Keywords: cell adhesion

Query Match 6.8%; Score 163; DB 2; Length 5376;

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Qy 75 GCTEAKDQEPRTVEHRMGPGLSLSYTFVCRQEDFCNNLVNSLPLWAPPPADPGS---- 130

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Qy 131 ---LRCPVCLSMEGCL-----EGTTEEICPKGTHTCYDGLLRGGGIFSNLRVQGM 180

Db 3295 EITLQCPNTSFTDCLPSCPSCNRCEVTSFSPSSCREGL-CNHGFVFESE---DKCV 3350

Qy 181 POPCNULLNGTQETGPVGMT---ENCNRKDFLTCHRTTITMTHGNLAQEPDWTTSNTE- 236

Db 3351 PRTQCGCKDARGAIPAGKTWTSKGCTQS--CACVEGN--IQCNFQCPPEPYKDNSEG 3406

Qy 237 -----MCEVGVCQETLL--- 249

Db 3407 SSTCTKITLQCPANTQVTSCLPCLPCLDPEGLCKDISPKVPSTCKGCGVCQSGYVLS 3466

Qy 250 -----LIDVGLTSTLVG--TKGCVTVG-----AQNSQKTTIHSPGVLIV 287

Db 3467 DKCVLRAECDCKDAQGALIIPAGKTWTSKGCTQS--CACVEGN--IQCNFQCPPEPYKDNSEG 3518

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Qy 338 GSPRM--TCPRGATHCYDGVII 356
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## RESULT 2

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 C:date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T30274  
 R:Laidlaw, M.; Wessel, G.M.  
 Development 120, 1325-1333, 1994  
 A:title: Cortical granule biogenesis is active throughout oogenesis in sea urchins.  
 A:Reference number: Z20803; MUID:94298531; PMID:8026340  
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Qy	140	EGCLEGTEETPCPKGTTTHCDGLLRGGGIFSNLRVQG--CMPQPQGNLLNGTQIEGPV197
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Db	834	-----DCGNNYCVWGSKCDGVSDCSN--GODESECPPTTSACPEGRVDCGNNYCVWGKCDG888
Qy	295	SSDLCSNASSSSVLLNLSLPQAAAPVGDG--QCPT--CV-----QPLGTCSGSGSPR-----341
Db	889	VSDCSNQDES-----GCPPTIVTCPAGRIDCGTNYCVUGARCDGVSDCSNGQDESGCPP943
Qy	342	--MTCPRGATHCYDGYIHLSC-----GGLSTKMSIOGCVAPSSFLLNHTRQIGIFSARE394
Db	944	AIVTCPAGRVDCGNNYCVWGSKCDGVSDCSNGQDEEGC-----SFSRCRS988
Qy	395	KRDVQPPASQHEGGGAGLESLL416
Db	989	RGDC-----EFFGTEAVESL1003

## RESULT 3

JN0561  
urokinase-type plasminogen activator receptor precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 31-Dec-1993 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: JN0561; #46977  
R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.  
Gene 125, 177-183, 1993  
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and induc  
A;Reference number: JN0560; MUID:93216119; PMID:8385052  
A;Accession: JN0561

A,Molecule type: mRNA  
A,Residues: 1-330 <KRA>  
A,Cross-references: UNIPROT:Q05588; UNIPARC:UPI0000137CC6; GB:L03545; NID:g163802; PIDN:R.;Reuning, U.; Little, S.P.; Dixon, E.P.; Johnstone, E.M.; Bang, N.U. Thromb. Res. 72, 59-70, 1993  
A,Title: Molecular cloning of cDNA for the bovine urokinase-type plasminogen activator  
A,Reference number: I46977; MUID:94167671; PMID:8122188  
A,Accession: I46977  
A,Status: translated from GB/EMBL/DDBJ  
A,Molecule type: mRNA  
A,Residues: 1-330 <REU>  
A,Cross-references: UNIPARC:UPI0000137CC6; GB:S70635; NID:g545770; PIDN:AAB30120.1; PID: C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology  
C,Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linka  
F,1-20/Domain: signal sequence #status predicted <SIG>  
F,21-300/Product: urokinase-type plasminogen activator receptor #status predicted <MAT>  
F,21-104/Domain: Ly-6 homology <LY6a>  
F,113-201/Domain: Ly-6 homology <LY6B>  
F,209-296/Domain: Ly-6 homology <LY6C>  
F,301-330/Domain: carboxyl-terminal propeptide #status predicted <PRO>  
F,28,72,179,189,279/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F,300/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly)(in mature fo

## RESULT 4

T16840  
hypothetical protein T10E10.4 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: T16840  
R/Geisel, C.  
submitted to the EMBL Data Library, October 1995  
A/Description: The sequence of *C. elegans* cosmid T10E10.  
A/Reference number: Z18588  
A/Accession: T16840  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA



Db 360 ECPHGRGTGLCHLKACISNPCNEGSNC-----DTNPVNGKRICTCPSGYTGPACS 410  
 Qy 330 QPIGTGSSGSPRM-----TCPRGATHCYDGVHLSGGGLSTKMSIQCVAPSSFL 381  
 Db 411 QDVDEOLGANREHAGKCLNTLGSFECQCLQGYT-----GPCCEIDVNECISNPCQND 465  
 Qy 382 NHTRQIGIF 390  
 Db 466 TCLDQIGEF 474  
 RESULT 6  
 VNHU  
 von Willebrand factor precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 C:Accession: A34480; S02377; A37139; S23676; A252298; A25366; S23618; A94  
 R; Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora  
 J. Biol. Chem. 264, 19514-19527, 1989  
 A:Title: Structure of the gene for human von Willebrand factor.  
 A:Reference number: A34480; MUID:90062044; PMID:2584182  
 A:Accession: A34480  
 A:Molecule type: DNA  
 A:Residues: 1-2813 <MAN>  
 A:Cross-references: UNIPROT:P04275; UNIPARC:UPI0000046823; EMBL:M25864  
 R; Bonthron, D.; Orkin, S.H.  
 Eur. J. Biochem. 171, 51-57, 1988  
 A:Title: The human von Willebrand factor gene. Structure of the 5' region.  
 A:Reference number: S02377; MUID:98111704; PMID:2828057  
 A:Accession: S02377  
 A:Molecule type: DNA  
 A:Residues: 1-177 <B02>  
 A:Cross-references: UNIPARC:UPI000017431A; EMBL:X06828  
 R; Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sora  
 Biochemistry 30, 253-269, 1991  
 A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and differ  
 A:Reference number: A37139; MUID:91105089; PMID:1988024  
 A:Accession: A37139  
 A:Molecule type: DNA  
 A:Residues: 990-1947 <MAD>  
 A:Cross-references: UNIPARC:UPI000016930B; GB:M60675; NID:g340357; PIDN:AAA61295.1; PID  
 A:Note: the authors translated the codon CGC for residue 156 as Gln  
 R; Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian,  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987  
 A:Title: Molecular cloning of the human gene for von Willebrand factor and identificatio  
 A:Reference number: S23676; MUID:87260814; PMID:3496594  
 A:Accession: S23676  
 A:Molecule type: DNA  
 A:Residues: 2731-2813 <COL>  
 A:Cross-references: UNIPARC:UPI000014240A; EMBL:M16945  
 R; Bonthron, D.; Orr, E.C.; Mitsock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.  
 Nucleic Acids Res. 14, 7125-7127, 1986  
 A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.  
 A:Reference number: A25298; MUID:87016349; PMID:3489923  
 A:Accession: A25298  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-2813 <BON>  
 A:Cross-references: UNIPARC:UPI000017431B; EMBL:X04385  
 R; Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 1839-1847, 1986  
 A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protei  
 A:Reference number: A91044; MUID:87004550; PMID:3019665  
 A:Accession: A25469  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>  
 A:Cross-references: UNIPARC:UPI000017431C; EMBL:X04146  
 A:Note: this sequence has been revised in reference A91056  
 R; Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 3074, 1986  
 A:Reference number: A91056  
 A:Accession: A25366  
 A:Molecule type: mRNA  
 A:Residues: 1021-1030 <VER2>

A:Cross-references: UNIPARC:UPI000017431D  
 A:Note: this is a revision to the sequence from reference A91044  
 R; Shelton-Inloes, B.B.; Broeze Jr., G.J.; Milewich, J.P.; Sadler, J.E.  
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987  
 A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeat  
 A:Reference number: S23618; MUID:87213253; PMID:3495266  
 A:Accession: S23618  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <SH2>  
 A:Cross-references: UNIPARC:UPI000016B30A; EMBL:M17588; NID:g799330; PIDN:AAA65940.1; P  
 A:Accession: S23645  
 A:Molecule type: protein  
 A:Residues: 23-56 <SH3>  
 A:Cross-references: UNIPARC:UPI000017431E  
 R; Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985  
 A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact  
 A:Reference number: A94060; MUID:86016708; PMID:2864688  
 A:Accession: A94060  
 A:Molecule type: mRNA  
 A:Residues: 'WA', 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873; 1289-1471, 'D', 1473  
 A:Cross-references: UNIPARC:UPI000017431F; UNIPARC:UPI0000174320  
 A:Note: the authors translated the codon TCG for residue 2168 as Cys  
 R; Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.  
 Biochemistry 25, 3164-3171, 1986  
 A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated d  
 A:Reference number: A90504; MUID:86269894; PMID:3488076  
 A:Accession: A90504  
 A:Molecule type: mRNA  
 A:Residues: 781-788, 'A', 790-1424 <SHB>  
 A:Cross-references: UNIPARC:UPI0000174321  
 R; Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.;  
 Science 228, 1401-1406, 1985  
 A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clone  
 A:Reference number: A44178; MUID:85244588; PMID:3874428  
 A:Accession: A44178  
 A:Molecule type: mRNA  
 A:Residues: 2621-2813 <GIN>  
 A:Cross-references: UNIPARC:UPI000016B307; EMBL:K03028; NID:g340308; PIDN:AAA61293.1; P  
 R; Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; v  
 Nucleic Acids Res. 13, 4699-4717, 1985  
 A:Title: Construction of cDNA coding for human von Willebrand factor using antibody pro  
 A:Reference number: S07363; MUID:85269603; PMID:3875078  
 A:Accession: S07363  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <VE3>  
 A:Cross-references: UNIPARC:UPI000014240A; EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PI  
 R; Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Livi  
 Cell 41, 49-56, 1985  
 A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a  
 A:Reference number: S23678; MUID:85201687; PMID:3873280  
 A:Accession: S23678  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <LYN>  
 A:Cross-references: UNIPARC:UPI000014240A; EMBL:K03028  
 R; Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.  
 Biochemistry 25, 3171-3184, 1986  
 A:Title: Amino acid sequences of human von Willebrand factor.  
 A:Reference number: A90505; MUID:86269895; PMID:3524673  
 A:Accession: A90505  
 A:Molecule type: protein  
 A:Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TIT>  
 A:Cross-references: UNIPARC:UPI0000174322  
 A:Note: 789-Thr was also found  
 R; Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.  
 Biochemistry 25, 3146-3155, 1986  
 A:Title: Human von Willebrand factor: a multivalent protein composed of identical subun  
 A:Reference number: A23464; MUID:86269892; PMID:3015199  
 A:Accession: A23464  
 A:Molecule type: protein  
 A:Residues: 764-773; 2803-2813 <CHO>  
 A:Cross-references: UNIPARC:UPI0000174323; UNIPARC:UPI0000174324

R;Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990  
A;Title: Identification of a cleavage site directing the immunochemical detection of mol  
A;Reference number: A36013; MUID:90349604; PMID:2385594  
A;Accession: A36013  
A;Molecule type: protein  
A;Residues: 1606-1617 <DEN>  
A;Cross-references: UNIPARC:UPI0000174325  
R;Fay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Ohlsson-Wilhelm, B.M.;  
Science 233, 995-998, 1986  
A;Title: Propolypeptide of von Willebrand factor circulates in blood and is identical to  
A;Reference number: A60913; MUID:86208144; PMID:3486471  
A;Accession: A60913  
A;Molecule type: protein  
A;Residues: 576-590 <FAY>  
A;Cross-references: UNIPARC:UPI0000174326  
C;Genetics:  
A;Gene: GDB:VWF  
A;Cross-references: GDB:119125; OMIM:193400  
A;Map position: 12p13.3-12p13.2  
A;Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1; 51  
5/1; 1724/1; 1771/1; 1819/1; 1874/1; 1888/3; 1948/1; 2021/3; 2086/1; 2200/1; 2266/3; 230  
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von  
C;Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-763/Product: von Willebrand antigen II #status predicted <NA1>  
F;34-386/Domain: type D repeat 1 <DD1>  
F;387-745/Domain: type D repeat 2 <DD2>  
F;698-700/Region: cell attachment (R-G-D) motif  
F;784-865/Domain: D' <DDD>  
F;788-833; 2216-2261/Region: duplication  
F;826-853; 2400-2515; 2544-2662/Region: duplication  
F;842-1130; 1934-2203/Region: duplication  
F;866-1241/Domain: type D repeat 3 <DD3>  
F;1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>  
F;1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>  
F;1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>  
F;1947-2295/Domain: type D repeat 4 <DD4>  
F;2296-2330/Domain: type B repeat 1 <VB1>  
F;2340-2365/Domain: type B repeat 2 <VB2>  
F;2375-2399/Domain: type B repeat 3 <VB3>  
F;2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>  
F;2507-2509/Region: cell attachment (R-G-D) motif  
F;2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>  
F;857;1231;1515;1574;2223;2290;2357;2400;2546;2585;2790/Binding site: carbohydrate (Asn)  
F;1147/Binding site: carbohydrate (Asn) (covalent) #status atypical  
F;1248;1255;1256;1468;1477;1487;1679;2298/Binding site: carbohydrate (Thr) (covalent) #  
F;1263;1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 5.58; Score 131.5; DB 1; Length 2813;  
Best Local Similarity 21.78; Pred. No. 0.27; Indels 135; Gaps 23;  
Matches 85; Conservative 39; Mismatches 132

Qy 18 GVALLCQFGTVQHVWVSDLPKNTSKDGLGQDPTL-----MLIE 63  
Db 2092 GANDFMLRDGTVDWT--LVQENTVQR-----PGQCQPILEQCLVPDSSHCQVLLP 2145

Qy 64 SGQVSLVLSKG-----CTEAKDQEPVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLP 118  
Db 2146 LFAECHKVLAPATFYAICQDQSCHEQVCE-----VIASAHLCRTNGVCVD----- 2192

Qy 119 LNAQPPADPGSLRCPVCLSNEGLEGTEIEICPKGTHCYDGLLRGG-----GIF--- 171  
Db 2193 -WR---TPDFCAMSPPSLVYNHCEG-----CPR---HC-DGNVSSCGDPHSPGCFPP 2239

Qy 172 SNLRVQG-CMPOPCNLLNGTQELGPGVMTNCNRKDFL-----TCHRTGTI 217  
Db 2240 DKVWLESCVPEEAC-----TQCLGEDGV-----QHOFLEAWVDHPQCICITCLSRKV 2289

Qy 218 MTHGNLAQEPDWTNT-EMCEVQ-----QVCBETLLIIDV-----GLT 256  
Db 2290 ----NCTTQCPQTKAFTGCLCEVARLRQADQCPEYECVCDPVSDDLPPVPHCERGLQ 2345

Qy 257 STLVGTKGCTVGAQNSQKTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLSLRPPQA 316  
Db 2346 PTLTN-----PBCRPNTFCARKECKRVSP-----SCPFR 2379

Qy 317 APVGDQRQCTCVQPLGTCSSGSPRMTCPRG 347  
Db 2380 LPTLRKTQC--CDEYECACNCVNSTVSCPLG 2408

RESULT 7  
Ti5840  
hypothetical protein C54G7.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: Ti5840  
R;Du, Z.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid C54G7.  
A;Reference number: Z18416  
A;Accession: Ti5840  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2946 <DUZ>  
A;Cross-references: UNIPARC:UPI000017B871; EMBL:U40410; NID:gl065453; PID:gl065455; PII  
C;Genetics:  
A;Gene: CESP:C54G7.3  
A;Introns: 16/1; 53/2; 92/1; 160/3; 295/1; 346/1; 392/1; 440/1; 475/3; 579/1; 615/3; 1-  
46/1; 2561/2; 2603/2; 2626/2; 2665/2; 2716/3; 2804/3; 2884/3

Query Match 5.58; Score 130; DB 2; Length 2946;  
Best Local Similarity 21.88; Pred. No. 0.36;  
Matches 98; Conservative 52; Mismatches 202; Indels 98; Gaps 24;

Qy 23 LCQFGTVQHVWVSDLPKNTSKDGLGQDPTL-----GLGQDPTLMLISGPOVSLVLSKG 76  
Db 1683 MCKFGDV---KCDPSEPVTPSPGGSGNLRECTGGSVCRGWCIC---PDPSIMVNRGI 1735

Qy 77 TEAKDQEPVTEHRMGPGLSL-----ISYTFVCRQEDFCNNLVNSLPWAPQ-PPA 126  
Db 1736 CIQSGPKPTLPPTPIQVPLPPOLPISVHVPOVTITKAQFF-----ITEAPL-APQGGKI 1790

Qy 127 DPQSLRC---PVCLSMEGCLGTEIEICPKGTHCYDGLLRGGIFSNLRVQCMQPQ 183  
Db 1791 VPQG-RGPIDVCVGGSCNIEGFC--LCPAGQQPSNSGRCEK-----FTTTSRQTLPST 1842

Qy 184 GCNLLNGTQIGVPGWTE--NCNRKQPLTCHRGTT---IMTHGNL---AOBPTDWTNT 235  
Db 1843 TTTQGTITTTTAPPTTSVFSFTIADLLSTRQPAFIEIPTHVPLTTTATQTDDECTAIG 1902

Qy 236 EMCEVGVQVQ-----ETLLLDVGLTSLVGTGKGCSTVGAQNSQKTT-IHSAP----- 282  
Db 1903 LICKGNTVCNKSQCQCPETVYLHHDGCVSPPEAARRKARKARKEATTAARLYSPGSECT 1962

Qy 283 -----PGVLVASYTHFCSSDLNCSASSSSVLLNSLPQAPAPVPCDQCPTCVQPLGTCSS 337  
Db 1963 QGQTCVGGSSACSFRKLCECPQDKSEISQGCVT--PRKLEVVPG-----ASC-NANTVCTK 2015

Qy 338 GSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQCVQAQPSFLLNHTQIGIFGAREKD 397  
Db 2016 GS---TCESGLCRCPQYIAVSG-----NCVALPMS-----TTPKMRV 2050

Qy 398 VQPASQHEGG-CAEGLESITWVGGLALAP 426  
Db 2051 IAKPLESCENGETCEGSGNCDYDTGCMCP 2080

## RESULT 8

S16148  
gene serrate protein precursor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 31-Dec-1991 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
C;Accession: S16148; S16878; A36666

R;Thomas, U.; Speicher, S.A.; Knust, E.  
Development 111, 749-761, 1991  
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co-  
A;Reference number: S16148; MUID:91347903; PMID:1840519  
A;Accession: S16148  
A;Molecule type: mRNA  
A;Residues: 1-1408 <THO1>  
A;Cross-references: UNIPROT:P18169; UNIPARC:UPI000017A1AA; EMBL:X56811  
R;Thomas, U.  
submitted to the EMBL Data Library, November 1990  
A;Reference number: S16878  
A;Accession: S16878  
A;Molecule type: mRNA  
A;Residues: 1-1351, T, 1353-1408 <THO2>  
A;Cross-references: UNIPARC:UPI000013588E; EMBL:X56811; NID:98563; PID:g8564  
R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Teakonas, S.  
Genes Dev. 4, 2188-2201, 1990  
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential fo  
A;Reference number: A36666; MUID:91099666; PMID:2125287  
A;Accession: A36666  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-15,20-26, 'A',28-1408 <FLE>  
A;Cross-references: UNIPARC:UPI0000498BA; GB:M35759; NID:g158605; PID:g158606  
C;Genetics:  
A;Gene: FlyBase:Ser  
A;Cross-references: FlyBase:Fgn0004197  
C;Keywords: Glycoprotein; transmembrane protein  
F;1-84/Domain: signal sequence #status predicted <SIG>  
F;85-1408/Product: gene serrate protein #status predicted <MAT>  
F;85-1221/Domain: extracellular #status predicted <EXT>  
F;283-316/Domain: EGF homology <EG01>  
F;319-348/Domain: EGF homology <EG02>  
F;355-388/Domain: EGF homology <EG03>  
F;395-488/Domain: EGF homology #status atypical <EG04>  
F;495-526/Domain: EGF homology <EG05>  
F;533-608/Domain: EGF homology #status atypical <EG06>  
F;615-645/Domain: EGF homology <EG07>  
F;652-683/Domain: EGF homology <EG08>  
F;690-720/Domain: EGF homology <EG09>  
F;727-796/Domain: EGF homology #status atypical <EG10>  
F;803-834/Domain: EGF homology <EG11>  
F;841-876/Domain: EGF homology <EG12>  
F;883-914/Domain: EGF homology <EG13>  
F;921-952/Domain: EGF homology <EG14>  
F;957-1060/Region: cysteine-rich  
F;1222-1246/Domain: transmembrane #status predicted <TM1>  
F;1247-1408/Domain: intracellular #status predicted <INT>  
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Ase

QY 285 VLVASYTHFCSSDLCSNASSSVLLNSLPQAA-----PVPGRQCPTCVQ 330  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 954 ILLSD-----PKSACQNAS-----NTISFYTALNRSONWLDTALTGRTEDDDNCNACV- 1001  
 QY 331 PLGTCTSGSGSPRMT--CPRGATHCYDGYIHLGGGLSTKMSIQG-----CVAQPSSFL 380  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1002 ----CENGTSRCTNLWC--GLPNCY-----KVDFLSKSNLSEGVCKQHVCVPALSETC 1049  
 QY 381 LNHETROI-GIFSAIRE-KRDVQPP-----ASQHEGGGA-- 410  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1050 LSSPCNVRGDCRALERSRRVAPPRLPAKSCWPNQAVVNENCARLTILLALERVGKASV 1109  
 QY 411 EGGLESLTWGVLAPAL 428  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1110 EGLCSL---VRVLLAAQL 1124

RESULT 9  
 T15881  
 hypothetical protein D1044.3 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: T15881  
 R;Pauley, A.  
 submitted to the EMBL Data Library, June 1994  
 A;Description: The sequence of C. elegans cosmid D1044.  
 A;Reference number: Z18423  
 A;Accession: T15881  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1895 <PAU>  
 A;Cross-references: UNIPARC:UPI000004CAE8; EMBL:U00065; NID:g495681; PID:g495684; PIDN:  
 A;Experimental source: strain Bristol N2  
 C;Genetics:  
 A;Gene: CSSP:D1044.3  
 A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 1  
 Query Match 5.4%; Score 127.5; DB 2; Length 1895;  
 Best Local Similarity 20.6%; Pred. No. 0.35;  
 Matches 73; Conservative 51; Mismatches 148; Indels 83; Gaps 15;

QY 22 LLCQFTVOHVWVKVDLPQWTPKNWSC----DSGLGCCQDTLMLES GPQVSLVSKGCT 77  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1121 LNCOLGTVSF-----NSQCITLASPGQNCQTSSQCIDN---SVMCMQMCT 1162  
 QY 78 EAKDQEPRVTEHRMGPLSLISVTFVCRQBDFCNNLVNSLFWAPDPAGSLRCPCVL 137  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1163 CNNN-----YKLVGYCVPITSSICQQ---TQTLVNNOCVLL-----SIVGETCI 1204  
 QY 138 SMEBCELGTTTEECPKGTHTCYDGLLRGGGIFSNLRVQCGMPQPCGN-----LL 189  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1205 ANQQCVGGA---MCNSGTQCTNGATAMYGCISSS-----SSSCSNSOVNSINGWCY 1253  
 QY 189 NGTOEI GPVGMENCRKDFELTCHRGTTIMTHGLAQEPDWTITSNTEMCEVQVCQETL 248  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1254 NTVQVGCSCSFSCQCLNN--AVCTNNICVSTFCVS-----CSTNQVCILSNQ 1298  
 QY 249 LLTDVGLTSLVTGKTGSTVGAQNSQ-KTIHSAPPGVLVASYTHFCSSDLCSNASSSSV 307  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1299 CYNVVISGQCVGSQQC----LSNSQCISSICCCPQGTQOSNGVCTGNNNNNQCQPNQV 1354  
 QY 308 LINSLEPQAAPVEDGRQCPTCVQPLGTCSSGSRPMTCPRGATHCYDGYIHLSGGG 362  
 :|:: |:: |:: |:: |:: |:: |:: |:: |:: |::  
 Db 1355 LINNOQYNTVSI--GFQCQFPQOCLGNSQCMNSMQCQPTGSTN-VNGYCOGGSGNG 1406

RESULT 10  
 T30075  
 hypothetical protein F57F4.4 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T30075



R;Miller, N.; Bradshaw, H.  
submitted to the EMBL Data Library, September 1996  
A;Description: The sequence of *C. elegans* cosmid F57F4.  
A;Reference number: Z20730  
A;Accession: T30075  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2090 <MIL>  
A;Cross-references: UNIPROT:Q94247; UNIPARC:UPI000007C44F; EMBL:U70856; PIDN:AAB09166.1  
A;Experimental source: strain Bristol N2; clone F57F4  
C;Genetics:  
A;Gene: CESP:F57F4.4  
A;Map position: 5  
A;Introns: 42/3; 117/2; 1962/3; 2025/1

```
Query Match          5.3%; Score 126.5; DB 2; Length 2090;
Best Local Similarity 17.1%; Pred. No. 0.46;
Matches 77; Conservative 60; Mismatches 182; Indels 131; Gaps 20;

QY 44 PKNTSCDSGLGCDTLMLESQVSLVSKGCTEAKDQPRVTEHRMGPGLSLISYTFV 103
DB 1390 PPPTSVDYAIACY-TGLYVNGVSTPVILG-----ACQGCASISLNTTLNGVATTATLYG 1444

QY 104 CROEDFCNNLVNSLPLWAPDPAGSLRCPVCLSMGCLGTEETEEICPKGTTTHCYDGLL 163
DB 1445 CDPSTVCQSL--NNNNWCASP--IPGVSGC--CCNTDCLDPPKNTKTPVSGFRKCFAGIY 1498

QY 164 ---RLRGGGIF-----SNLRVQGCMPQPCNLLNGTQIEIGPVGMT----- 200
DB 1499 AOGKATGSEIFCPGKCAISOATLNQDPVAIFGCVPTQFCRLEWYDECKPLPYDTTGTG 1558

QY 201 -----ENC-----NRKDF-LTCHRGTTIMTHGNLAQEPDW----- 230
DB 1559 CCNYYNVCNVDLAGYGGKINTSPVTNFRDYPACFSGLYV---NNMPISIAGQACKGE 1615

QY 231 -----TTSENTEMCVGVQCE-----TLLLLIDVGLTSLVGTGKC----- 265
DB 1616 CASATLSTMYNGALTWNATVTCDPVSTCYQLGMNNNCTTIENGLSGCCSTDACLDPTVS 1675

QY 266 -----STVGAQ---NSQKTTIHSAPGVVLVASYTHFCSSDLNCSA 302
DB 1676 PPRTPNPLKCYVGLQSTYNSLSLGAETVCSGQCASLTGIVGFNVTTY-HCVADTICKSL 1734

QY 303 SSSSVLLNSLPPQAAVPGDRQCPT-CVQPLGTCSSGSPRM-----TCPRGATHCYDGYI 356
DB 1735 -----EIKDTCRPLWSREVTAACCNADNCLKDPNVKPGPAVLDPFPPTACYQGLL 1786

QY 357 HLSGGGLSTKWSIQGCVAPQSPSFLNHTQ 386
DB 1787 -VNNQTYGAPLTLLQGCYGCDCASITISTIQ 1815
```

## RESULT 11

T30074  
hypothetical protein F57F4.3 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30074  
R;Miller, N.; Bradshaw, H.  
submitted to the EMBL Data Library, September 1996  
A;Description: The sequence of *C. elegans* cosmid F57F4.  
A;Reference number: Z20730  
A;Accession: T30074  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2153 <MIL>  
A;Cross-references: UNIPROT:Q94246; UNIPARC:UPI000007CB3D; EMBL:U70856; PIDN:AAB09166.1  
A;Experimental source: strain Bristol N2; clone F57F4  
C;Genetics:  
A;Gene: CESP:F57F4.3  
A;Map position: 5  
A;Introns: 42/3; 117/2; 1962/3; 2025/1

```
Query Match          5.3%; Score 126.5; DB 2; Length 2153;
Best Local Similarity 17.1%; Pred. No. 0.47;
Matches 77; Conservative 60; Mismatches 182; Indels 131; Gaps 20;

QY 44 PKNTSCDSGLGCDTLMLESQVSLVSKGCTEAKDQPRVTEHRMGPGLSLISYTFV 103
DB 1390 PPPTSVDYAIACY-TGLYVNGVSTPVILG-----ACQGCASISLNTTLNGVATTATLYG 1444

QY 104 CROEDFCNNLVNSLPLWAPDPAGSLRCPVCLSMGCLGTEETEEICPKGTTTHCYDGLL 163
DB 1445 CDPSTVCQSL--NNNNWCASP--IPGVSGC--CCNTDCLDPPKNTKTPVSGFRKCFAGIY 1498

QY 164 ---RLRGGGIF-----SNLRVQGCMPQPCNLLNGTQIEIGPVGMT----- 200
DB 1499 AOGKATGSEIFCPGKCAISOATLNQDPVAIFGCVPTQFCRLEWYDECKPLPYDTTGTG 1558

QY 201 -----ENC-----NRKDF-LTCHRGTTIMTHGNLAQEPDW----- 230
DB 1559 CCNYYNVCNVDLAGYGGKINTSPVTNFRDYPACFSGLYV---NNMPISIAGQACKGE 1615

QY 231 -----TTSENTEMCVGVQCE-----TLLLLIDVGLTSLVGTGKC----- 265
DB 1616 CASATLSTMYNGALTWNATVTCDPVSTCYQLGMNNNCTTIENGLSGCCSTDACLDPTVS 1675

QY 266 -----STVGAQ---NSQKTTIHSAPGVVLVASYTHFCSSDLNCSA 302
DB 1676 PPRTPNPLKCYVGLQSTYNSLSLGAETVCSGQCASLTGIVGFNVTTY-HCVADTICKSL 1734

QY 303 SSSSVLLNSLPPQAAVPGDRQCPT-CVQPLGTCSSGSPRM-----TCPRGATHCYDGYI 356
DB 1735 -----EIKDTCRPLWSREVTAACCNADNCLKDPNVKPGPAVLDPFPPTACYQGLL 1786

QY 357 HLSGGGLSTKWSIQGCVAPQSPSFLNHTQ 386
DB 1787 -VNNQTYGAPLTLLQGCYGCDCASITISTIQ 1815
```

## RESULT 12

C42125  
trophozoite cysteine-rich surface antigen 72 - *Giardia lamblia* (fragment)  
N;Alternate names: CRP72  
C;Species: *Giardia lamblia*  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
C;Accession: C42125  
R;Adam, R.D.; Yang, Y.M.; Nash, T.E.  
Mol. Cell. Biol. 12, 1194-1201, 1992  
A;Title: The cysteine-rich protein gene family of *Giardia lamblia*: loss of the CRP170  
A;Reference number: A42125; MUID:92186850; PMID:1545800  
A;Accession: C42125  
A;Molecule type: DNA  
A;Residues: 1-677 <ADA>  
A;Cross-references: UNIPROT:Q7M3R4; UNIPARC:UPI000001785CF; GB:M83934; NID:gl59123  
A;Experimental source: trophozoites  
A;Note: sequence extracted from NCBI backbone (NCBIN:88443, NCBI:P:88444); this ORF is  
C;Keywords: surface antigen

```
Query Match          5.1%; Score 122.5; DB 2; Length 677;
Best Local Similarity 20.9%; Pred. No. 0.27;
Matches 71; Conservative 30; Mismatches 121; Indels 117; Gaps 19;

QY 107 EDFCENLVNSLPLWAPQPPA-----DPGSLRCPVC-----LSMEGC---LEGTT 147
DB 40 DGFGR-----PFGSQAAAGCTKAGGAALDKWTATCEKGGDYFLPMGCGYKTTDGGP 93

QY 148 EEICPKG-----TTHCYDGLRLRGGGIFSNLRVQGCMPQPG-----CNLLNGTQIEIGPVG 198
DB 94 SEICTRAEGGLCTEC-----KTANGLFKN---PAATPEKSGSEICLCSIDINGADGYTGVA 144

QY 199 MTENCNR-----KDFLTCHR--GTTIMTHGNLAQEPD-----D 229
DB 145 NCAQCKTSDNSKGAATCTACQAGYKDFQACSKODGTCLTCTETSAACQCTCEPEGYLKGD 204

QY 230 WTTSENTEMC-----EVGVQVCELTLLIDVGLTSLVGTGKCVTVGAQN 272
```



Db 205 KSCVNNNGCTGNTYADPESGKCLPCNTIDQACTQ-----CEVDSSTTKPK-CTNCGGQK 257  
QY 273 SOKTTIHSAPPGLVLSYTHFCS-----SDLCNSASSSSVLLNSLPQQAAPVPGDRQCP 326  
Db 258 MVKTAI-----DGTTCVDANGCATSNVDGSHFLNDGSKTCLICSD---DSLEANKGTP 310  
QY 327 TCVPQLGCTSSGSPRMTCPRGATHCYDGYIHLSSGGGLST 365  
Db 311 GC-----KTCKNGAKETC-----SECLDGYNSNGGTVT 341  
RESULT 13  
T09059  
notch4 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09059  
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.  
submitted to the EMBL Data Library, October 1997  
A;Description: Sequence of the mouse major histocompatibility locus class III region.  
A;Reference number: Z16543  
A;Accession: T09059  
A;Status: preliminary; translated from GB/EMBL/DBU  
A;Molecule type: DNA  
A;Residues: 1-1964 <ROW>  
A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:G2564945;  
C;Genetics:  
A;Gene: notch4  
A;Map position: 17  
A;Map: introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67  
1679/3; 1729/1; 1761/3  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
C;Keywords: receptor, signal transduction  
F;514-545/Domain: EGF homology <EGF>  
Query Match 5.1%; Score 122.5; DB 2; Length 1964;  
Best Local Similarity 20.4%; Pred. No. 0.83;  
Matches 113; Conservative 36; Mismatches 161; Indels 243; Gaps 31;  
QY 17 PGVQALLCQRG---TVQH-----VWK-----VSDLPQRWTPK 45  
Db 263 PGFTGLDCENPNPDCVRHQCGQNGATCLDGLDTVCLCPKTKWGDCEIDCEARGPPR 322  
QY 46 NTSCDSGLGCDTLMLESBPQSVLSLVS---KGTEAKDQEPVTEHRMGPGLSLI--- 98  
Db 323 ---CRNGTQONT-----ASFHCVCVSGHGGACENLDCAAT---CAPGSTCIDRV 371  
QY 99 -SYT-----FVCRQEDFC-----NNLVNSLPL-----TDWTSNTMCEVG 119  
Db 372 GSFSCLCPPGRTGLCHLEDWCLSQPCHVNAQCSTNPLTGTCLICQPGYSGSTCHQDLD 431  
QY 120 ---WAPOPPA-----DPGLRCPVCLSMGCLGTT-----EEICPKG 154  
Db 432 EQMAQQGSPCEHGGSCINTPGSFNCL-----CLPGYTGRCEADHNECLSQPCHPG 484  
QY 155 TT-----HCY--DGLLRLLRGGIFSNLRVQCMPPQCN-----LLNGTQEIIPVG 198  
Db 485 STCLDLAATHCLCPPLG-----EGRUCEVEVNECTSNPCLNQACHDLINGFQCLCLPG 539  
QY 199 MTENCNRKDFLTCHRGTTIMTHGNLAQEP-----TDWTSNTMCEVG 241  
Db 540 FTGARCEKMDCEC--SSTPCANGGRCDQPGAFYCECLPGFPHCEKEVEDECLSDPCPVG 598  
QY 242 QVQOET-----LLLDVGLTSLVTKGCTVGAQNSQKT--THSAPPGLVLSYTHFCS 295  
Db 599 ASCLDLPGAFCLCRPGFTGQLCEVPPLCTPNMCPGQQCQGEHRAP-----C- 646  
QY 296 SDLCNSASSSSVLLNSLPQQAAP--VPGDRQCP----- 326  
Db 647 --LC-----PDGSPCVCVAEDNCPCHGHCQBSLCVDCGWTGPCETELG 690  
QY 327 -----TC-VQPLG---TCSSGSPRMTCPRGATHCYDGYIHLSSGGGLSTKMSIQG 371

Db 691 GCISTFPCARGGTCHPQPSGYNCTCPAGYMLGTCSEETACHSGPC-LNGGSCSIRPEGYS 749  
QY 372 CVAQSSSFLNHT 384  
Db 750 CYCLPS-----HT 757  
RESULT 14  
S40992  
hypothetical protein K04H4.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 03-May-1994 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
C;Accession: S40992  
R;Ainscough, R.  
submitted to the EMBL Data Library, October 1993  
A;Reference number: S40991  
A;Accession: S40992  
A;Molecule type: DNA  
A;Residues: 1-738 <AIN>  
A;Cross-references: UNIPROT:P34504; UNIPARC:UPI000017BA8E; EMBL:Z27078  
C;Genetics:  
A;Introns: 62/1; 140/1; 206/1; 226/1; 269/1; 308/1; 536/1; 604/1; 668/1  
Query Match 5.1%; Score 121.5; DB 2; Length 738;  
Best Local Similarity 20.3%; Pred. No. 0.35;  
Matches 94; Conservative 43; Mismatches 170; Indels 155; Gaps 21;  
QY 48 SCDSGLGCDTLMLESBPQSVLSLKGCTEAKDQEPVTEHRMGPGLSLSTFVCRQE 107  
Db 329 TCSNGLCCAGTSTVK-----CLDGSDAVGACIPSTGDCGGVQSVYCGSG 376  
QY 108 DFCNNLVNSLPLWAPQPADPGSLRCPV--CLSMEGCLEGTTEEICPKGTT----- 156  
Db 377 YTCIT-----GNICCPINSCPNGGEVLGPTINGLCPTGTVVQGNLCCSA 420  
QY 157 HCVDGLLRGGGIFSNLRVQG--CMPQPGCNLLNG-----TQBIG----- 195  
Db 421 TCTDGSSTGLPS-----VNGVCI--DGYSLTNGVCCPASVTCTDDEISIGPCTGTGFGNG 470  
QY 196 --PVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTMCEVGQ---VCQETLL 249  
Db 471 GCPAGYACDSNVQNCPPVRYT-----DESCQVGPDAIDGLCPPGYV 511  
QY 250 LIDV-----GLTSTLVGTRGCTVGAQNSQKTTHSAPPGLVLSYTHFCS 297  
Db 512 VVYIPNSPLITNGVNPGTCLDLOCTTGLCLTANQIGCDTATDA--GTCPTGYTCFTNAG 569  
QY 298 LCNSASSSSVLLNSLPQQAAPVPG-----DRQCP---TCVQ---PLGTCSSG--- 338  
Db 570 ICCSTTTFSRLRIGNSRQMAQKENYGRPLHSYMPRKCPSGDGTAVSGCFPPNGSCGTGYECV 629  
QY 339 -SPRMTCPRGATHCYDGYIHLSSGGSLSTKMSIQGCVAPSSFLNHTHQIFISAREKD 397  
Db 630 SSLNLCCPPQPPOTFFSPGNNG-----FNINNNRFGSLMSPR-- 670  
QY 398 VQPPAS--QHEG---GGAEGLESILTGWGLALAPALWGVVC 434  
Db 671 --PIGARCOLDGEVQAEGLSMCHAGVCCQCSPIAYTQGIAC 710  
RESULT 15  
B88553  
protein K04H4.2b [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Accession: B88553  
R;anonymouse, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C.el  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

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A:Accession: B88553
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-739 <STO>
A:Cross-references: UNIPARC:UPI000016415C; GB:chr_III; PIDN:CAA81588.1; PID:g3878238; GS
C:Genetics:
A:Gene: K04H4.2b
A:Map position: 3

Query Match
Best Local Similarity    5.1%; Score 121.5; DB 2; Length 739;
Matches      94; Conservative   43; Mismatches 170; Indels 155; Gaps    21;
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Qy 48 SCDSGLGCQDTLMLIESGPQSVLSKGTGEAKDQEPRVTEHRMGPGSLISITYFVCROE 107  
Db :|||:|||::--CLDGSDAVGACIPCSTGDGCGGVQSVYICSGS 377

Qy 108 DFCNNLVNSLPWAPQPADPSLRCPV---CLSMEGCLGGTTEEI CPKTT----- 156  
Db :|||:|||::--GNICPFINSPNGSEVLPTINGLCFTGYTVQGNLCCSA 421

Qy 378 YTCYT-----GNICPFINSPNGSEVLPTINGLCFTGYTVQGNLCCSA 421

Qy 157 HCVDGLRLRGGGIFSNLRVOG-CMPQPGCNILNG-----TOEIG----- 195  
Db :|||:|||::--VNGVCI-DGVSITNGVCCPASVTCTDEISIGPCTGTGFNG 471

Qy 196 --PVGMTENCRKDPLTCHRTGITIMTHGNLAQEPTDWTTSNTEMCEVGQ----VQETLL 249  
Db :|||:|||::--DESCQVGPAIDGLCLPPGYV 512

Qy 472 GC PAGYACDSNQYNCCPVRYT-----DSCQVGPAIDGLCLPPGYV 512

Qy 250 LIDV-----GLTSLTGTCSTVGQAQNSOKTTIHSA PPLVASVTFHCSSD 297  
Db :|||:|||::--DRQCP---TCVQ---PLGTCSGS----- 338

Qy 513 VVIPI NSPLITNGVNFGTCIDLQTITGLCLTANIQIGDCDTATDA--GTCPGTGTCFNAG 570

Qy 298 LCNSASSSVLLNSLPQAAVPVG-----DROCP---TCVQ---PLGTCSGS----- 338  
Db :|||:|||::--DSCQVGPAIDGLCLPPGYV 512

Qy 571 ICCSTTTFSRIRLIGNSRMAQKNYGRPLHSYMPRKPSGDTA VS GCFPNGSCGTGYECV 630

Qy 339 -SPRMTCPRGATHCYDGYITHLSGGGLSTRKMSIOGCCVAQPSSFLNHTROI GFISAREKD 397  
Db :|||:|||::--FMINNRFGLSLMSPR-- 671

Qy 631 SSLNLCCFPQQPOTFFSFPGNNNG-----FMINNRFGLSLMSPR-- 671

Qy 398 VQPPAS--QHEG---GAAGLESLTWGVLALAPALMWGVVC 434

Qy 672 --PIGARCOLDGRCVGOAGLSMCHAGVCOCSPAIVTOGIAC 711

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2006, 09:21:42 ; Search time 300 seconds  
(without alignments)  
1347.439 Million cell updates/sec

Title: US-10-727-619-2

Perfect score: 2381

Sequence: 1 MSAVLLALIGFILPLGVQ.....WGVLALPALMGWVCPSC 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2381	100.0	437	2	Q9HDA5 HUMAN	Q9hda5 homo sapien
2	2370	99.5	437	2	Q8N6Q3 HUMAN	Q8n6q3 homo sapien
3	2360	99.1	437	2	Q96QH1 HUMAN	Q96qh1 homo sapien
4	1179	49.5	817	2	Q8R2S8 MOUSE	Q8r2s8 mus musculus
5	1108	46.5	248	2	Q711Q2 HUMAN	Q711q2 homo sapien
6	687	28.9	145	2	Q8NCV9 HUMAN	Q8ncv9 homo sapien
7	523	22.0	212	2	Q9D0T8 MOUSE	Q9d0t8 mus musculus
8	378.5	15.9	246	2	Q810N3 MOUSE	Q810n3 mus musculus
9	366	15.4	153	2	Q78K55 MOUSE	Q78k55 mus musculus
10	341.5	14.3	249	2	Q9BPY7 HUMAN	Q9bp7 homo sapien
11	341.5	14.3	267	2	Q715R2 HUMAN	Q715r2 homo sapien
12	330.5	13.9	267	2	Q9BY14 HUMAN	Q9by14 homo sapien
13	298.5	12.5	250	2	Q924B5 RAT	Q924b5 rattus norv
14	294	12.3	196	2	Q8CFJ5 MOUSE	Q8cfj5 mus musculus
15	293	12.3	253	2	Q7TQNZ CRIGR	Q7tn2 cricetus
16	282	11.8	250	2	Q9JMI7 MOUSE	Q9jmi7 mus musculus
17	252	10.6	246	1	LYPD4 MOUSE	Q8bvp6 mus musculus
18	247	10.4	246	1	LYPD4 BOVIN	Q321d3 bos taurus
19	240	10.1	246	1	LYPD4 HUMAN	Q6uwn0 homo sapien
20	163	6.8	5376	1	ZAN MOUSE	Q88799 mus musculus
21	154	6.5	5374	2	Q99ND0 MOUSE	Q99nd0 mus musculus
22	152	6.4	1577	2	Q4SPE0 TETNG	Q4spe0 tetraodon n
23	148.5	6.2	1264	2	Q26632 STRPU	Q26632 stronglyloce
24	148.5	6.1	1408	2	Q4RX38 TETNG	Q4rx38 tetraodon n
25	144.5	6.1	1637	2	Q9XSU8 BOVIN	Q9xsu8 bos taurus
26	144.5	6.1	5146	2	Q8SPM4 BOVIN	Q8spm4 bos taurus
27	143.5	6.0	4260	2	Q4T3T2 TETNG	Q4t3t2 tetraodon n
28	142	6.0	330	1	UPAR BOVIN	Q05588 bos taurus
29	142	6.0	555	2	Q54RC6 D1CDI	Q54rc6 dictyosteli
30	142	6.0	950	2	Q802C1 XENLA	Q802c1 xenopus lae
31	142	6.0	2602	2	Q7PSV8 ANOGA	Q7psv8 anopheles g

32 141.5 5.9 1280 2 Q6QHS1 LYTVA Q6qhs1 lytechinus  
33 141 5.9 555 1 D8E7 D1CDI D8e7 dictyosteli  
34 140.5 5.9 2428 2 Q816X6 BOOMI Q816x6 boophilus m  
35 139 5.8 1642 2 Q515F7 ENTHI Q515f7 entamoeba h  
36 139 5.8 2284 2 Q9VFG1 DROME Q9vfg1 drosophila  
37 138.5 5.8 1302 1 LTBP3 HUMAN LTbp3 homo sapien  
38 138 5.8 822 2 Q2Q426 MACMU Q2q426 macaca mula  
39 137.5 5.8 1656 2 Q50S97 ENTHI Q50s97 entamoeba h  
40 137.5 5.8 4699 2 Q9V383 DROME Q9v383 drosophila  
41 136.5 5.7 966 2 Q22378 CAEEL Q22378 caenorhabdi  
42 136.5 5.7 2531 1 NOTC1 MOUSE Notc1 mus musculu  
43 135 5.7 919 2 Q61V24 CAEBR Q61v24 caenorhabdi  
44 134.5 5.6 635 2 Q7QP07 GIALA Q7qp07 giardia lam  
45 133.5 5.6 729 2 Q4RQK5 TETNG Q4rqk5 tetraodon n

## ALIGNMENTS

### RESULT 1

ID Q9HDA5\_HUMAN PRELIMINARY; PRT; 437 AA.  
AC Q9HDA5;  
DT 01-MAR-2001, integrated into UniprotKB/TREMBL.  
DT 07-FEB-2006, entry version 12.  
DE Cell surface receptor (PRV1) (Polycychemia rubra vera 1).  
GN Name=PRV1; ORFNames=UNQ595;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Temerinac S., Klippel S., Strunck E., Roder S., Lubbert M., Lange W.,  
RA Azemar M., Meinhardt G., Schaefer H.E., Pahl H.L.;  
RT "Cloning of PRV-1, a novel member of the UPAR receptor superfamily,  
RT which is overexpressed in polycychemia rubra vera.";  
RL Blood 95:2569-2576(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chul C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H., Goddard A.D.,  
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor  
RT vector.";  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AF146747; AAC00895.1; -; mRNA.  
DR EMBL; AY358932; AAC08291.1; -; mRNA.  
DR EMBL; BT020111; AAV38914.1; -; mRNA.  
GO; GO:0004872; F:receptor activity; IEA.

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DR InterPro; IPR001526; LY6_UPAR.
DR Pfam; PF00021; UPAR_LY6; 2.
KW Receptor.
SQ SEQUENCE 437 AA; 46363 MW; 3D40648723843865 CRC64;

Query Match 100.0%; Score 2381; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 5.9e-176;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAVLLALLGLFTLPVQVALLCQFGTVQHVWVKVSDLPKQWTPKNTSCDSGLGCQDTLM 60
DB 1 MSAVLLALLGLFTLPVQVALLCQFGTVQHVWVKVSDLPKQWTPKNTSCDSGLGCQDTLM 60

QY 61 LIESGQVSLVLSKGTCTEAKDQEPRTVEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
DB 61 LIESGQVSLVLSKGTCTEAKDQEPRTVEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120

QY 121 APOPPADPSGLRCPVCLSMGCGLEGTEETICPKGTHCYDGLRLRGGGIFSNLRVQGM 180
DB 121 APOPPADPSGLRCPVCLSMGCGLEGTEETICPKGTHCYDGLRLRGGGIFSNLRVQGM 180

QY 181 POPGCLLNGTQIEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTNTNCEV 240
DB 181 POPGCLLNGTQIEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTNTNCEV 240

QY 241 GQVCQETLLLDVGLTSTLVGTGKCSVGAQNSQKTTIHSAPPGLVASYTHFCSSDLN 300
DB 241 GQVCQETLLLDVGLTSTLVGTGKCSVGAQNSQKTTIHSAPPGLVASYTHFCSSDLN 300

QY 301 SASSSSVLLNSLPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360
DB 301 SASSSSVLLNSLPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360

QY 361 GGLSTKMSIQGCVAPQSSFLNHTROIIGIFSAREKRDVQPASQHEGGGAGLESITWGV 420
DB 361 GGLSTKMSIQGCVAPQSSFLNHTROIIGIFSAREKRDVQPASQHEGGGAGLESITWGV 420

QY 421 GLALAPALMWGVVCPSC 437
DB 421 GLALAPALMWGVVCPSC 437

RESULT 2
Q8NEQ3 HUMAN
ID Q8NEQ3_HUMAN PRELIMINARY; PRT; 437 AA.
AC Q8NEQ3
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Polycythemia rubra vera 1.
GN Names=PRV1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21357611; PubMed=11465086;  
RA DOI=10.1002/1521-4141(200105)31:5<1301::AID-IMMU1301>3.0.CO;2-J;  
RA Kissel K., Santoso S., Hofmann C., Stroneck D., Bux J.;  
RT "Molecular basis of the neutrophil glycoprotein NBI (CD177) involved  
RL in the pathogenesis of immunoneutropenia and transfusion reactions";  
CC Eur. J. Immunol. 31:1301-1309(2001).  
CC -----  
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CC -----  
DR EMBL: AJ290452; CAC44459.1; -; mRNA.  
DR InterPro: IPR001526; LY6\_UPAR.  
DR Pfam: PF00021; UPAR\_LY6; 2.  
KW SIGNAL.  
FT CHAIN 1 21 Potential.  
FT SIGNAL 22 437 NBI protein.  
SQ SEQUENCE 437 AA; 46335 MW; 823D4F784986A42F CRC64;  
Query Match 99.1%; Score 2360; DB 2; Length 437;  
Best Local Similarity 99.1%; Pred. No. 2.5e-174;  
Matches 433; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MSVALLALGFIPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDPTLM 60  
Db 1 MSPVLLALLGFIPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDPTLM 60  
Qy 61 LIESGQVSLVSLKGTCEAKQDPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPW 120  
Db 61 LIESGQVSLVSLKGTCEAKQDPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPW 120  
Qy 121 APQPPADPGSLRCPVCLSMGCLSGTTEICPKGTHCYDGLRLRGCGIFSNLRVQGM 180  
Db 121 APQPPADPGSLRCPVCLSMGCLSGTTEICPKGTHCYDGLRLRGCGIFSNLRVQGM 180  
Qy 181 PQPCNLLNGTQIEGPVGMTECNCRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
Db 181 PQPCNLLNGTQIEGPVGMTECNCRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
Qy 241 GQVQETILLIDVLTSTLVGTGCGSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLN 300  
Db 241 GQVQETILLIDVLTSTLVGTGCGSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLN 300  
Qy 301 SASSSVLLNSLPQAPVPGDRCPCVPLGTCSSGSPMTCPRGATHCYDGYIHLG 360  
Db 301 SASSSVLLNSLPQAPVPGDRCPCVPLGTCSSGSPMTCPRGATHCYDGYIHLG 360  
Qy 361 GGLSTKMSIQCVAPQSSFLNHTROIGIFSAREKRDVQPPASOHEGGAGLESITWGV 420  
Db 361 GGLSTKMSIQCVAPQSSFLNHTROIGIFSAREKRDVQPPASOHEGGAGLESITWGV 420  
Qy 421 GLALAPALWGWVCPSC 437  
Db 421 GLALAPALWGWVCPSC 437  
RESULT 4  
Q8R2S8\_MOUSE PRELIMINARY; PRT; 817 AA.  
AC Q8R2S8;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 22.  
DE CD177 antigen.  
GN Name=Cd177;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.

RC 10 month old virgin mouse. Taken by biopsy.;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.  
RC 10 month old virgin mouse. Taken by biopsy.;  
RG NIH MSC Project,  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL: BC027283; AA27283.1; -; mRNA.  
DR Ensembl: ENSMUSG00000052212; Mus musculus.  
DR MGI: MGI:1916141; 1190003K14Rik.  
DR MGI: MGI:1916141; Cd177.  
DR InterPro: IPR001526; LY6\_UPAR.  
DR Pfam: PF00021; UPAR\_LY6; 4.  
DR SQU SEQUENCE 817 AA; 87091 MW; F22A8B073D6F7C60 CRC64;  
Query Match 49.5%; Score 1179; DB 2; Length 817;  
Best Local Similarity 53.6%; Pred. No. 1.7e-82;  
Matches 230; Conservative 59; Mismatches 122; Indels 18; Gaps 7;  
Qy 19 VQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDPTLMIESGQVSLVSLKGTCE 78  
Db 397 LDALCQHGTLKTTQDISKLPLQWTAGOKICNVGEGCDTLMLENGEQVNLVLTGCTT 456  
Qy 79 AKQDEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPWAPQPPADPGSLRCPVCL 138  
Db 457 AKQDEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPWAPQPPADPGSLRCPVCL 516  
Qy 139 MEGCLEGTTEICPKGTHCYDGLRLRGCGIFSNLRVQGMCPQPCNLLNGTQIEGVPV 198  
Db 517 EQAC-ENAPQVCPAGSTHCYSGVLSLGGGIIIDLKVGCGMSQPCNLLNGTQIEGVP 575  
Qy 199 MTENC---NRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTECEVQVQVQCTLLIDVGL 255  
Db 576 VSERCSPSETTELSYCYGVNMFELNGFAEPVFKWTAPGSGVCAPEADICQETLLIDVGL 635  
Qy 256 TSTLVGTGCGSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLNCSASSSVLLNSLPQ 315  
Db 636 KSAFLGSGCGSSPGAQDNIGVIFSRPLGMLVASYTRFCSHLNCGADSSSVLLSILPRP 695  
Qy 316 AAPVPGDRQCPCTCVPLGTCSSGSPMTCPRGATHCYDGYIHLGSGGLSTKMSIQGCV 375  
Db 696 DVPPGVDGQCPMCEVLEFGSCKS-TDSVTCPRGATHCYKGDIALOGGGLTTRVSIQCNAP 754  
Qy 376 PSSFLNHTROIGIFSAREKRDVQPPASOHEGGAGGAE-----LESITWGVGL-ALAPAL 428  
Db 755 PIKPLGDSKTIGIFSAEBSNY-----RHEDDVTSAPSLAWTLRLSAMLGLSALLSSL 809  
Qy 429 WGWVCPSC 437

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Db      810 YAG-ICPLC 817
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RESULT 5
ID Q71102 HUMAN PRELIMINARY; PRT; 248 AA.
AC Q71102;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE NBI glycoprotein precursor.
GN Name=NBI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Kessel K., Scheffler S., Bux J.;
RT "mRNA of NBI (HNA-2a) negative individuals.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP Kessel K., Scheffler S., Kessel K.;
RA Bux J., Scheffler S., Bux J.;
RT "Molecular basis of the NBI (HNA-2a)-negative phenotype.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
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EMBL: AJ310433; CAC83724.1; -; mRNA.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 248 AA; 27165 MW; E385D3DB37C51581 CRC64;
Query Match 46.5%; Score 1108; DB 2; Length 248;
Best Local Similarity 97.1%; Pred. No. 1.3e-77;
Matches 203; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSALLLALGFLPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDITLM 60
DB 1 MSPVLLALLGFLPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDITLM 60
QY 61 LIESGPQVSLVLSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
DB 61 LIESGPQVSLVLSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
QY 121 APQPPADPGSLRCPVCLSMGCLGTTTCPCKTHCYDGLLRGGGIFSNLRVQGCM 180
DB 121 APQPPADPGSLRCPVCLSMGCLGTTTCPCKTHCYDGLLRGGGIFSNLRVQGCM 180
QY 181 POPCNLLNGTOETGPVGMTECNCRKDPL 209
DB 181 POPVCNLLNGTOETGPVGMTECNCRKDPL 209
RESULT 6
ID Q8NCV9 HUMAN PRELIMINARY; PRT; 145 AA.
AC Q8NCV9;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Glycoprotein NBI precursor.
GN Name=NBI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Kessel K., Scheffler S., Bux J.;
RT "mRNA of NBI (HNA-2a) negative individuals.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP Kessel K., Scheffler S., Kessel K.;
RA Bux J., Scheffler S., Bux J.;
RT "Molecular basis of the NBI (HNA-2a)-negative phenotype.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
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EMBL: AJ310433; CAC83724.1; -; mRNA.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 145 AA; 15709 MW; EF7FB498A8B39053 CRC64;
Query Match 28.9%; Score 687; DB 2; Length 145;
Best Local Similarity 90.3%; Pred. No. 3e-45;
Matches 131; Conservative 0; Mismatches 4; Indels 10; Gaps 1;
QY 1 MSALLLALGFLPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDITLM 60
DB 1 MSPVLLALLGFLPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDITLM 60
QY 61 LIESGPQVSLVLSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
DB 61 LIESGPQVSLVLSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
QY 121 APQPPADPGSLRCPVCLSMGCLG 145
DB 121 APQPPADP-----MMGAAEG 135
RESULT 7
ID Q9D0T8 MOUSE PRELIMINARY; PRT; 212 AA.
AC Q9D0T8;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 24.
DE 16-day embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:1190003K14 product: hypothetical protein, full insert sequence.
DE (Fragment).
GN Names=Cdl177;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
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RA Georgii-Hemming P., Gingeras T.R., Gojibori T., Green R.E.,  
RA Guisticich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madena M., Marchionni L.,  
RA Matsuda H., Matuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottaqui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rest B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RT Science 309:1559-1563 (2005).  
RL [3]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC PubMed=16141073; DOI=10.1126/science.1112009;  
RX RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566 (2005).  
RL [4]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC PubMed=22334681; PubMed=12466851; DOI=10.1038/nature01266;  
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schirnl L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Guisticich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numa K., Okido T., Pavan W.J., Perte G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,  
RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hasegawa W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Watanston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RT Nature 420:563-573 (2002).  
RL [5]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schirnl L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guisticich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RT Nature 409:685-690 (2001).  
RL [6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RT Genome Res. 10:1617-1630 (2000).  
RL [7]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RT Genome Res. 10:1757-1771 (2000).  
RL [8]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa K., Saito H., Saito R., Sakai K., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL; AK004472; BAB23319.2; -; mRNA.  
DR MGI; MGI:1916141; Cdl177.  
DR KWP Hypothetical protein.  
FT NON TER 1 1  
SQ SEQUENCE 212 AA; 22172 MW; 0C4B2B2A17096C4E CRC64;  
Query Match 22.0%; Score 523; DB 2; Length 212;  
Best Local Similarity 50.2%; Pred. No. 2.4e-32;  
Matches 110; Conservative 29; Mismatches 66; Indels 14; Gaps 5;

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QY 226 EPTDWTTSNTMCEVGVQVCOETILLIDVGLTSLVETKGCSTVGAQNSQKTTIHSAPPGV 285
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 1 EPVKWTAPGSOVCAPDEICQETILLIDVGQKSAFLGSKGCSGPAQDNIGVSIFSLPGM 60
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 286 LVASYTHFCSSDLNCSASSSVLLNSLPQAAVPVGGDRQCTCVQPLGTCSSGSPMTCP 345
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 61 LVASYTKFCSSHLNCGADSSSVLLSLPRDPVPPGVDVQCPMCELVFSGCKS-TDSVTCP 119
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 346 RGATHCYDGVYIHLSSGGLSTKMSIQGCVAOPSSFLNLNHTROIIGFSAREKRDVQPPASQ 405
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 120 RGATHCYGKDALQGGGLITRVSLOGCMAPPIKPLGDSKSTIIGFSAEBSNY-----RH 174
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 406 EGGGAEG-----LESITGWGVL-ALAPALMWGVVCPSC 437
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 175 EDDVTSAPSLAWTLRLSNAWMLGLSALLSLIYAG-ICPLC 212
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 8
Q810N3 MOUSE
ID Q810N3 MOUSE PRELIMINARY; PRT; 246 AA.
AC Q810N3
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DE Hypothetical protein BC049730.
DE Hypothetical protein BC049730.
GN Name=BC049730;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Director MGC Project;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
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CC EMBL; BC049730; AA049730.1; -; mRNA.
DR Ensembl; ENSMUSG00000045587; Mus musculus.
DR MGI; MGI:2681843; BC049730.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR_LY6_1.
KW Hypothetical protein
SQ SEQUENCE 246 AA; 26554 MW; 0874C995EC94E06 CRC64;

Query Match 15.9%; Score 378.5; DB 2; Length 246;
Best Local Similarity 50.6%; Pred. No. 2.4e-20;
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Best Local Similarity 37.8%; Pred. No. 4.5e-21;
Matches 90; Conservative 37; Mismatches 96; Indels 15; Gaps 6;

QY 203 CNRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTEMC- -VGQVCOETLLIDVGLTSTLV 260
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 18 CPCSDTLNCOEBSVMKFGQNFSTSIEMVQTVGSEKNGKEMCOEIFLIDVGEKSLIL 77
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 261 GTKGCSVTGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSVLLNSLPQAAVP 320
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 78 GTKGITTVGPKR-KKTDVFPSPGPGIVSASVHFCDTDLNCSASTKVLKLLKLSYNEP 136
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 321 GRCQCTCVQPLGTCSSGSPMTCPRGATHCYDGYIHLSSGGLSTKMSIQGCVAOPSSFL 380
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 137 GTTKCPVCLDFKGCNCTESNHTLCPKD-TKCYAASLGVHGGDLSAIFSGCLNSSTYL 195
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 381 LANHTROIIGIFSAREKRDVQPPASQHEGGGAEG- - -ESLTGWGVLALAPALMWGVVC 434
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 196 LNNQNTIGIISIKETDESNTLS-----SQGLLVFSILLTWFGFL-LALCLQRSVLC 246
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 9
Q78KC5 MOUSE
ID Q78KC5 MOUSE PRELIMINARY; PRT; 153 AA.
AC Q78KC5
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Cd177 protein.
DE Name=Cd177;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RG NIH MGC Project;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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CC EMBL; BC005615; AA005615.1; -; mRNA.
DR MGI; MGI:1916141; Cd177.
SQ SEQUENCE 153 AA; 16087 MW; 6DEAAF297B4FC579 CRC64;

Query Match 15.4%; Score 366; DB 2; Length 153;
Best Local Similarity 50.6%; Pred. No. 2.4e-20;
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SQ SEQUENCE 267 AA; 28532 MW; 59CAF4951E2AB760 CRC64;
Query Match 14.3%; Score 341.5; DB 2; Length 267;
Best Local Similarity 34.2%; Pred. No. 3.6e-18;
Matches 76; Conservative 38; Mismatches 93; Indels 15; Gaps 7;

QY 209 LTHRGTTIMTHGNAQEPDWTTSNTEMCVGVQVCOETLLIDVGLTSLVGTGCGSTV 268
DB 44 LYCKQLGLSMTVEADPA-NMFWTTEVEVETCDKALCOETLLIKAGTETAILATKGIPE 102

QY 269 GAQNSOKTTI--HSAPGVULVASYTHFCSSDLNCSASSSSVLLNSLPQAPVPGDRQCP 326
DB 103 G---EEAITIVQHSPPGLVITSYNYCEDSFCDKSLSQFWEFSETTASTVSTTLHCP 159

QY 327 TCVOPLGTCSGSPRMTCPRGATHCYDGYIHLSSGGLSTRKMSIQGCVAPQSSFLNHTHQ 386
DB 160 TCV-ALGTCTFS-APSLPCPNMTGTRCYQVKLEITGGGIESSEVFGKCTAMIGCRMLSGILA 217

QY 387 IGIFSARE----KRDVQPPASOHEGGAGGLESITWGVGLAL 424
DB 218 VGMFVREACPHQLLTQPRKTEN--GATCLPIPVWGLQLLL 256

RESULT 12
Q9BY14 HUMAN PRELIMINARY; PRT; 267 AA.
AC Q9BY14_HUMAN integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Scleroderma-associated autoantigen.
GN Name=TEX101;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang J., Ni Z., Xie Y., Zhong L., Lei H., Shi L., Zhao G., Hu L.,
RA Kong X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AF241268; AAK28327.1; -; mRNA.
DR Ensembl; ENSG00000131126; Homo sapiens.
DR LinkHub; Q9BY14; -.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
SQ SEQUENCE 267 AA; 28617 MW; 30D15F7BCA40ACC5 CRC64;

Query Match 13.9%; Score 330.5; DB 2; Length 267;
Best Local Similarity 33.8%; Pred. No. 2.6e-17;
Matches 75; Conservative 38; Mismatches 94; Indels 15; Gaps 7;

QY 209 LTHRGTTIMTHGNAQEPDWTTSNTEMCVGVQVCOETLLIDVGLTSLVGTGCGSTV 268
DB 44 LYCKQLGLSMTVEADPA-NMFWTTEVEVETCDKALCOETLLIKAGTETAILATKGIPE 102

QY 269 GAQNSOKTTI--HSAPGVULVASYTHFCSSDLNCSASSSSVLLNSLPQAPVPGDRQCP 326
DB 103 G---EEAITIVQHSPPGLVITSYNYCEDSFCDKSLSQFWEFSETTASTVSTTLHCP 159

QY 327 TCVOPLGTCSGSPRMTCPRGATHCYDGYIHLSSGGLSTRKMSIQGCVAPQSSFLNHTHQ 386
DB 160 TCV-ALGTCTFS-APSLPYNGTTCYQVKLEITGGGIESSEVFGKCTAMIGCRMLSGILA 217

QY 387 IGIFSARE----KRDVQPPASOHEGGAGGLESITWGVGLAL 424
DB 218 VGMFVREACPHQLLTQPRKTEN--GATCLPIPVWGLQLLL 256
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RESULT 13
Q924B5 RAT PRELIMINARY; PRT; 250 AA.
AC Q924B5_RAT integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Glycoprotein TEC-21.
DE Name=Tex101;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar;
RX MEDLINE=21542636; PubMed=11686435;
RA Halova I., Draberova L., Draber P.;
RT "New monoclonal antibodies to rat testicular antigen, TEC-21.";
RL Polia Biol. (Praha) 47:180-182(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar;
RX MEDLINE=21668242; PubMed=11809740; DOI=10.1093/intimm/14.2.213;
RA Halova I., Draberova L., Draber P.;
RT "A novel lipid raft-associated glycoprotein, TEC-21, activates rat
RT basophilic leukemia cells independently of the type 1 Fc epsilon
RT receptor.";
RL Int. Immunol. 14:213-223(2002).
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CC -----
EMBL; AF347056; AK58911.1; -; mRNA.
DR Ensembl; ENSRNOG0000020057; Rattus norvegicus.
DR RGD; 621373; Tex101.
DR GO; GO:0045121; C:lipid raft; IMP.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
SQ SEQUENCE 250 AA; 27004 MW; CFF31D13C980AC4C CRC64;

Query Match 12.5%; Score 298.5; DB 2; Length 250;
Best Local Similarity 30.9%; Pred. No. 7.2e-15;
Matches 71; Conservative 41; Mismatches 95; Indels 23; Gaps 8;

QY 19 VQALLCOFGTVQHVVKVSDLP---QWTPKNTSCDGLGCDTLLMLIES-GPQVSLVLSK 74
DB 23 VQNIYCE---VSRTLSEDPNPGTFNNTSKAEKCNPGECQETVLLIKAGETKAILASK 79

QY 75 GCTEAKDQEPRTVEHRMGPGLSLISYTFVCRQEDFCNNLVN-SLPLWAPQPPAD---PGS 130
DB 80 SCVPGQAGTMTFVOYTAPPGLVALSYSNYC-NDSLNNRNRLASILQAPETATSNMGA 138

QY 131 LRCPVCLSMEGCLEGTTETIEICPKGTHCYDGLLRCGGIFSNLRVQCGMPQPGCNLNG 190
DB 139 RHCTCLALEPCCSAPSMP-CANGTTQCYHGKIELSGGMDSVVHVKGCTTAIGRLMAK 197

QY 191 TQEIGPVGMTECNKRKDFLTCRGTMTTHGNLAQEPDWTTSNTECEV 240
DB 198 MESVGPMTVAKTCSYQSFL-----HPRMAEIGASWMTSLWLVELE 237

RESULT 14
Q8CFJ5 MOUSE PRELIMINARY; PRT; 196 AA.
AC Q8CFJ5_MOUSE integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Hypothetical protein MGC48079.
GN Name=MGC48079;
```

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus gland;  
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko V., Bonfard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]

## NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus gland;  
RA Strausberg R.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC037749; AAH37749.1; -; mRNA.  
DR Ensembl: ENSMUSG0000058717; Mus musculus.  
DR InterPro: IPR001526; LY6 UPAR.  
DR Pfam: PF00021; UPAR LY6; 1.  
KW Hypothetical protein.

SQ SEQUENCE 196 AA; 20969 MW; 3575C7D73237486 CRC64;

Query Match 12.3%; Score 294; DB 2; Length 196;  
Best Local Similarity 36.3%; Pred. No. 1.2e-14;  
Matches 66; Conservative 32; Mismatches 78; Indels 6; Gaps 4;

QY 257 STLVTGKCTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLNSLPQA 316

Db 20 SLILASKGSKAKSKSVNDVQVFGGPGIIVTASVHFCTELCNANSTSVLKNVLS 79

QY 317 APVPGDRQCTCQVPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGCVAQP 376

Db 80 SSGQGSITQCPVCLHFRGSCSOHTKFLCPKD-TRCYPSDMTVEGGGLKNFFSLDGLANS 138

QY 377 SSFLLNHTROIIGIFSAREKEDVQPPASQHEGGAGLESITWGVGL-ALAPALWGVVCP 435

Db 139 AKNLLSKQTSIGIFSVVE---VSNPGSSKSPSRVVASILLTWMGLRALLSLYAG-ICP 194

QY 436 SC 437

Db 195 LC 196

## RESULT 15

Q7TQN2 CRIGR

ID Q7TQN2\_CRIGR PRELIMINARY; PRT; 253 AA.

AC Q7TQN2;

DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2003, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Lipid raft-associated glycoprotein TEC-21.  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Cricetidae; Cricetinae; Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;  
RA Charvatova L., Tumova M., Draber P.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AY309070; AAP73441.1; -; mRNA.

DR InterPro: IPR001526; LY6 UPAR.

DR Pfam: PF00021; UPAR LY6; 1.

SQ SEQUENCE 253 AA; 26978 MW; A1BB49698B2589A7 CRC64;

Query Match 12.3%; Score 293; DB 2; Length 253;  
Best Local Similarity 32.5%; Pred. No. 1.9e-14;  
Matches 78; Conservative 41; Mismatches 83; Indels 38; Gaps 12;

QY 218 MTHGNLAQ-----EPT---DMTT--SNTMCEVGVQVCOETLLLLIDV-GLTS 257

Db 16 VSHQTLAQSLQCAVSKVLRLEDDPSRTFNWTSKPKVETCNPGELCQETVLLIKAEGTKT 75

QY 258 TLVGTGKCTVGAQNSOKTTI--HSAPPGVLVASYTHFCSSDLNCSASSSSVLLNSLPQ 315

Db 76 AVVASKGCA---SREIEAVTFIQYTPPGVIAISYNYCNSLNCN--NSKNVSLFWKPPD 130

QY 316 ---AAPVPGDRQCTCQVPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC 372

Db 131 TTATSKTLGALSCTPCV-ALGSCSS-APSPMCANSTTQCYGKIELSGGMDSVLHIKGC 188

QY 373 VAQPSFLLNHTROIIGIFSAREKRD----VQPPASQHEGGAGLESITWGVGLALAPAL 428

Db 189 TTAIGCELMAAITSVGPMVKETCSYHSLQPP--RKAESPASGRSTSLWVLELLPAVL 246

Search completed: July 11, 2006, 09:29:54

Job time : 303 secs

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GenCore version 5.1.9  
Copyright (C) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: July 11, 2006, 09:21:17 ; Search time 195 Seconds  
(without alignments)  
1024.634 Million cell updates/sec  
Title: US-10-727-619-2  
Perfect score: 2381  
Sequence: 1 MSALLLALLGFLPLPGVQ.....WGVLALAPALWGVVCPSC 437  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2589679 seqs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqp1990s:*					2: geneseqp1990s:*				
3: geneseqp2000s:*					3: geneseqp2000s:*				
4: geneseqp2001s:*					4: geneseqp2001s:*				
5: geneseqp2002s:*					5: geneseqp2002s:*				
6: geneseqp2003as:*					6: geneseqp2003as:*				
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9: geneseqp2005s:*					9: geneseqp2005s:*				
10: geneseqp2006s:*					10: geneseqp2006s:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	2381	100.0	437	3	Aay87750 Human PRV				
2	2381	100.0	437	3	Aay66737 Membrane-				
3	2381	100.0	437	3	Aay96733 PRO1863,				
4	2381	100.0	437	4	Aau12404 Human PRO				
5	2381	100.0	437	4	Aab70851 Human PRV				
6	2381	100.0	437	4	Aab5260 Human PRO				
7	2381	100.0	437	5	Aau83672 Human PRO				
8	2381	100.0	437	5	ABG92707 Human sec				
9	2381	100.0	437	5	ABG91359 Novel hum				
10	2381	100.0	437	5	ABG31399 Human PRO				
11	2381	100.0	437	5	ADY31902 Novel hum				
12	2381	100.0	437	6	ABU72375 Novel hum				
13	2381	100.0	437	6	ABU58075 Human PRO				
14	2381	100.0	437	6	ABU59153 Novel hum				
15	2381	100.0	437	6	ABU80865 Human sec				
16	2381	100.0	437	6	ABU82665 Human sec				
17	2381	100.0	437	6	ABU17848 Novel hum				
18	2381	100.0	437	6	ABU60584 Human sec				
19	2381	100.0	437	6	ABU80819 Human PRO				
20	2381	100.0	437	6	ABO33785 Novel hum				
21	2381	100.0	437	6	ABU13966 Human PRO				
22	2381	100.0	437	6	ABU81102 Human PRO				
23	2381	100.0	437	6	ABU72551 Novel hum				

24	2381	100.0	437	6	ABU66802	Human PRO
25	2381	100.0	437	6	ABG73312	Human PRO
26	2381	100.0	437	6	ABU59883	Novel sec
27	2381	100.0	437	6	ABU59300	Human sec
28	2381	100.0	437	6	ABO25997	Human PRO
29	2381	100.0	437	6	ABO25073	Human sec
30	2381	100.0	437	6	ABU82128	Novel hum
31	2381	100.0	437	6	ABU59006	Human sec
32	2381	100.0	437	6	ABU60811	Human sec
33	2381	100.0	437	6	ABU92384	Novel hum
34	2381	100.0	437	6	ABU59449	Novel hum
35	2381	100.0	437	6	ABU67078	Human sec
36	2381	100.0	437	6	ABU81234	Human PRO
37	2381	100.0	437	6	ABU92215	Novel hum
38	2381	100.0	437	6	ABU10921	Human PRO
39	2381	100.0	437	6	ABU81673	Novel hum
40	2381	100.0	437	6	ABU88612	Human sec
41	2381	100.0	437	6	ABO34126	Human PRO
42	2381	100.0	437	6	ADA45985	Novel hum
43	2381	100.0	437	6	ADA76416	Human PRO
44	2381	100.0	437	6	ABJ72308	Human PRO
45	2381	100.0	437	6	ADA19066	Human PRO

ALIGNMENTS

RESULT 1  
AAY87750  
ID AAY87750 standard; protein; 437 AA.  
XX  
AC AAY87750;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Human PRV-1 protein.  
XX  
KW PRV-1; human; polycythaemia rubra vera; PRV; antiproliferative;  
KW treatment; detection; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN DE19849044-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 23-OCT-1998; 98DE-01049044.  
XX  
PR 23-OCT-1998; 98DE-01049044.  
XX  
PA (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.  
XX  
PI Pahl H, Temerinac S;  
DR WPI: 2000-319347/28.  
DR N-PSDB; AAL2396.  
PT New polycythemia rubra vera-related polypeptide useful for diagnosis and  
for developing therapeutic antibodies.  
PS Claim 6; Fig 2; 6pp; German.  
XX  
XX This invention describes a novel PRV-1 protein (I) detected in humans  
suffering from the condition polycythaemia rubra vera (PRV). The product  
of the invention has antiproliferative activity. The encoding nucleic  
acid sequence is used to express recombinant PRV-1 polypeptides and as a  
source of antisense sequences that can be expressed in vivo for treatment  
of PRV. (I) is used to raise specific mono or polyclonal antibodies and  
these are used to diagnose PRV (by detecting (I), or its epitopes, in  
immunoassays) or for treatment of PRV (optionally when coupled to a  
cytotoxin). This sequence represents the human PRV-1 protein described in  
the method of the invention



[illegible]

PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI; 2000-072883/06.  
DR N-PSDB; AA265083.  
XX  
XX Membrane-bound proteins and related nucleotide sequences.  
XX  
XX Claim 12; Fig 250; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC nucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences

CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
SQ Sequence 437 AA;  
Query Match 100.0%; Score 2381; DB 3; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.1e-172; Indels 0; Gaps 0;  
Matches 437; Conservative 0; Mismatches 0;  
Qy 1 MSAVLLALALGFLPLPGVQALLCQFGTVQHVWKVSDLPKQWTPKNTSCDGLGCDPTLM 60  
Db 1 MSAVLLALALGFLPLPGVQALLCQFGTVQHVWKVSDLPKQWTPKNTSCDGLGCDPTLM 60  
Qy 61 LIESGPQVSLVSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSPLW 120  
Db 61 LIESGPQVSLVSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSPLW 120  
Qy 121 APOPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRGGLFNSLRVQCGM 180  
Db 121 APOPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRGGLFNSLRVQCGM 180  
Qy 181 PQPCNLLNGTQEIGPVGMTECNCRKDFLTCHRGTTIMTHGNLAQEPTDWTSTNCEV 240  
Db 181 PQPCNLLNGTQEIGPVGMTECNCRKDFLTCHRGTTIMTHGNLAQEPTDWTSTNCEV 240  
Qy 241 GQVCQETLLIDVGLTSTLVGTGCGSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLN 300  
Db 241 GQVCQETLLIDVGLTSTLVGTGCGSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLN 300  
Qy 301 SASSSSVLLNSLPQAPVPGDQCPTCVPLGTCCSSGSPRMTCPRGATHCYDGYIHLG 360  
Db 301 SASSSSVLLNSLPQAPVPGDQCPTCVPLGTCCSSGSPRMTCPRGATHCYDGYIHLG 360  
Qy 361 GGLSTKMSIQGCVAPQSSFLNHTROIQIFSAEKRDVQPPASQHEGGGAGLESLSLW 420  
Db 361 GGLSTKMSIQGCVAPQSSFLNHTROIQIFSAEKRDVQPPASQHEGGGAGLESLSLW 420  
Qy 421 GLALAPALMWGVVCPSC 437  
Db 421 GLALAPALMWGVVCPSC 437  
RESULT 3  
ID AAY96733 standard; protein; 437 AA.  
XX  
AC AAY96733;  
XX  
DT 26-SEP-2000 (first entry)  
XX  
DE PRO1863, a novel transmembrane protein.  
XX  
KW PRO1863; secreted protein; transmembrane protein; recombinant production;  
XX gene therapy.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..15  
XX FT /label= Signal\_peptide  
XX FT Modified-site 46..49  
XX FT Modified-site /note= "N-glycosylation site"  
XX FT Modified-site 51..54  
XX FT Modified-site /note= "Glycosaminoglycan attachment site"  
XX FT Modified-site 54..59  
XX FT Modified-site /note= "N-myristoylation site"  
XX FT Modified-site 75..80  
XX FT Modified-site /note= "N-myristoylation site"  
XX FT Modified-site 141..146  
XX FT Modified-site /note= "N-myristoylation site"  
XX FT Modified-site 154..159

FT /note= "N-myristoylation site"  
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FT 189. .192  
FT /note= "N-glycosylation site"  
FT 198. .203  
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FT 243. .260  
FT Domain  
FT /label= Transmembrane\_domain  
FT 254. .259  
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FT 261. .266  
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FT 359. .362  
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FT 360. .365  
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FT 388. .393  
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FT 408. .413  
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FT 419. .424  
FT /note= "N-myristoylation site"  
FT  
XX WO200036102-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 01-DEC-1999; 99WO-US028634.  
XX  
XX 16-DEC-1998; 98US-0112851P.  
XX 16-DEC-1998; 98US-0113145P.  
XX 22-DEC-1998; 98US-0113151P.  
XX 12-JAN-1999; 99US-0115558P.  
XX 12-JAN-1999; 99US-0115565P.  
XX 12-JAN-1999; 99US-0115733P.  
XX 09-FEB-1999; 99US-0119341P.  
XX 10-FEB-1999; 99US-0119537P.  
XX 12-FEB-1999; 99US-0119655P.  
XX 02-JUN-1999; 99WO-US012252.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;  
PI Garney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2000-431586/37.  
XX N-PSDB; AAA51263.  
XX  
XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a  
XX transmembrane polypeptide.  
XX  
XX Claim 12; Fig 10; 154pp; English.  
XX  
XX This is PRO1863, a novel transmembrane protein. The invention concerns  
XX novel secreted and transmembrane proteins, designated PRO polypeptides.  
XX CC The cDNA and gene sequences are useful in the recombinant production of  
XX CC PRO polypeptides, as a hybridization probe to screen libraries to isolate

CC cDNAs with sequence identity to PRO polypeptides or to map the gene  
CC encoding the PRO polypeptides and analyzing genetic disorders. The  
CC cDNA/gene can also be used to produce transgenic animals useful for the  
CC development and screening of therapeutically useful reagents. They can  
CC also be used in gene therapy, e.g. to replace a defective gene  
XX  
SQ Sequence 437 AA;  
  
Query Match 100.0%; Score 2381; DB 3; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.1e-172;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MSAVLLALLGFIPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLM 60  
Db |||||  
1 MSAVLLALLGFIPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLM 60  
  
QY 61 LIESGPOVSLVLSKGCTEAKQEPVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSIPLW 120  
Db |||||  
61 LIESGPOVSLVLSKGCTEAKQEPVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSIPLW 120  
  
QY 121 APQPPADPGSLRCPVCLSMEGCLEGTTEICPKGTHCYDGLLRGGGIFSNLRVQGCM 180  
Db |||||  
121 APQPPADPGSLRCPVCLSMEGCLEGTTEICPKGTHCYDGLLRGGGIFSNLRVQGCM 180  
  
QY 181 PPGCNLLNGTQEIIGPVGNTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTNTSEMCEV 240  
Db |||||  
181 PPGCNLLNGTQEIIGPVGNTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTNTSEMCEV 240  
  
QY 241 GOVCOETLLIDVGLTSTLVGKSTVGAQNSQKTIHSAPGVLVASVTHFCSSDLN 300  
Db |||||  
241 GOVCOETLLIDVGLTSTLVGKSTVGAQNSQKTIHSAPGVLVASVTHFCSSDLN 300  
  
QY 301 SASSSSVLLNSLPQAAVPVGDRCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
Db |||||  
301 SASSSSVLLNSLPQAAVPVGDRCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
  
QY 361 GGLSTKMSIQGCVAOPSPSFLNHTROIIGIFSAREKRDVQPPASQHEGGGAEGLESITWGV 420  
Db |||||  
361 GGLSTKMSIQGCVAOPSPSFLNHTROIIGIFSAREKRDVQPPASQHEGGGAEGLESITWGV 420  
  
QY 421 GLALAPALWVGVCPCSC 437  
Db |||||  
421 GLALAPALWVGVCPCSC 437  
  
RESULT 4  
AAU12404  
ID AAU12404 standard; protein; 437 AA.  
XX  
AC AAU12404;  
XX  
XX 24-OCT-2001 (first entry)  
XX  
XX Human PRO1181 polypeptide sequence.  
XX  
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
KW A-peptide; factor VIIA; gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO200140466-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 01-DEC-2000; 2000WO-US032678.  
XX  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028564.  
XX 02-DEC-1999; 99WO-US028565.

PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI; 2001-408281/43.  
DR N-PSDB; AAS21476.  
XX  
XX  
XX Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.  
XX  
XX Claim 12; Fig 466; 813pp; English.  
XX  
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear uricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy  
XX  
XX Sequence 437 AA;  
SQ

Query Match 100.0%; Score 2381; DB 4; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.1e-172;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSVALLALLGFIPLPGVQALLCQFCTVQHVWVSDLPQWTPKNTSCDGLGCGQDTLM 60  
DB 1 MSVALLALLGFIPLPGVQALLCQFCTVQHVWVSDLPQWTPKNTSCDGLGCGQDTLM 60  
QY 61 LIESGPOVSLVLSKGTCEAKDQEPRTVEHRMGPGLSLISYTFVCRQEDFCNNLVNSPLW 120  
DB 61 LIESGPOVSLVLSKGTCEAKDQEPRTVEHRMGPGLSLISYTFVCRQEDFCNNLVNSPLW 120  
QY 121 APOPPADPGSLRCPVCLSMGCLGTTTETEECPKGTTHCYDGLLRGGGIFSNLRVQGM 180  
DB 121 APOPPADPGSLRCPVCLSMGCLGTTTETEECPKGTTHCYDGLLRGGGIFSNLRVQGM 180  
QY 181 PQPCNLLNGTQBIGPVGMTENCNKRDLFCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
DB 181 PQPCNLLNGTQBIGPVGMTENCNKRDLFCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
QY 241 GQVCOETLLILIDVGLTSTLVGTGKCSVGAQNSQKTIHSAPPGVIVASYTHFCSSDLN 300  
DB 241 GQVCOETLLILIDVGLTSTLVGTGKCSVGAQNSQKTIHSAPPGVIVASYTHFCSSDLN 300  
QY 301 SASSSSVLLNSLPPQAAAPVPGDRQCTCQVPLGTCSGSPRMTCPRGATHCYDGYIHLG 360  
DB 301 SASSSSVLLNSLPPQAAAPVPGDRQCTCQVPLGTCSGSPRMTCPRGATHCYDGYIHLG 360  
QY 361 GGLSTKMSIQGCVAPSSFLNHTRQIGIFSAREKRDVQPPASQHEGGAGLESLETWGV 420  
DB 361 GGLSTKMSIQGCVAPSSFLNHTRQIGIFSAREKRDVQPPASQHEGGAGLESLETWGV 420  
QY 421 GLALAPALMWGVVCPSC 437  
DB 421 GLALAPALMWGVVCPSC 437

## RESULT 5

AAB70851

ID AAB70851 standard; protein; 437 AA.

XX AC

XX AAB70851;

XX DT

XX 29-JUN-2001 (first entry)

XX DE

XX Human PRV-1 protein.

XX KW

XX PRV-1; human; hemostatic; polycythemia rubra vera; antisense therapy;

XX KW treatment; diagnosis; pancytopenia; bone-marrow; blood; growth factor;

XX KW pancytopenia; hematopoietic system disorder.

XX OS

XX Homo sapiens.

XX XX

XX DE19947010-A1.

XX PD

XX 05-APR-2001.

XX XX

XX 30-SEP-1999; 99DE-01047010.

XX XX

XX 30-SEP-1999; 99DE-01047010.

XX XX

XX (UYFR-) UNIV FREIBURG.

XX PI

XX Pahl H;

XX XX

XX WPI; 2001-246167/26.

XX DR

XX N-PSDB; AAF61560.

XX XX

XX New cloned PRV-1 gene associated with polycythemia rubra vera, e.g.

XX PT useful for preparing antisense molecules or polypeptides for treatment or

XX PT diagnosis of disorders of the hematopoietic system.

XX XX

```

PS Claim 3; Fig 2; 10pp; German.
XX
CC This invention describes a novel cloned PRV-1 gene (I) which has
CC hemostatic activity and is associated with polycythemia rubra vera (PRV).
CC (I) is useful for: (1) producing a recombinant PRV-1 polypeptide; (2)
CC producing antisense molecules useful for diagnosis and treatment of PRV;
CC (3) preparing medicaments for treating pancytopenias and pancytopathies
CC of the bone-marrow and blood. The polypeptide is useful: (1) as a growth
CC factor for inducing hematopoietic stem cells to form erythroid colonies;
CC (2) for preparing medicaments for treating pancytopenias and
CC pancytopathies of the bone-marrow and blood; (3) for treating and/or
CC multiplying autologous cells and/or established cell lines ex vivo or in
CC vitro; and (4) for producing antibodies useful for diagnosis of PRV or
CC other disorders of the hematopoietic system. This sequence represents the
CC human PRV-1 protein described in the invention
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVLLALLGLFTPLPGVQALLCQFGTVQHVWVKVSDLPROWTPKNTSCDSGLGCQDTLM 60
DB 1 MSVLLALLGLFTPLPGVQALLCQFGTVQHVWVKVSDLPROWTPKNTSCDSGLGCQDTLM 60
QY 61 LTESGPQSVLSLKGCTEAKDQPRVTEHRMGPLSLISYTFVCROEDFCNNLVNSLPLW 120
DB 61 LTESGPQSVLSLKGCTEAKDQPRVTEHRMGPLSLISYTFVCROEDFCNNLVNSLPLW 120
QY 121 APOPPADPSLRCPVCLSMEGCLEGTTTEICPKGTHCYDGLRLRGGGIFSNLRVQGM 180
DB 121 APOPPADPSLRCPVCLSMEGCLEGTTTEICPKGTHCYDGLRLRGGGIFSNLRVQGM 180
QY 181 PQPGCNLLNGTQIGVPGVTENCRKDFLTCHRGTTIMTHGNLAQPTDWTTSNTEMCV 240
DB 181 PQPGCNLLNGTQIGVPGVTENCRKDFLTCHRGTTIMTHGNLAQPTDWTTSNTEMCV 240
QY 241 GOVCQETLLIDVGLTSTLVGTCSTVGAGNSQKTTIHSAPPGVLVASYTHFCSDDLGN 300
DB 241 GOVCQETLLIDVGLTSTLVGTCSTVGAGNSQKTTIHSAPPGVLVASYTHFCSDDLGN 300
QY 301 SASSSSVLLNSLPQAPVPGDRQCPTCVPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
DB 301 SASSSSVLLNSLPQAPVPGDRQCPTCVPLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360
QY 361 GGLSTWMSIQGCVAPQSSFLNHTROIGTIFSAEREKRDVQPASQHEGGGAEGLSTWGV 420
DB 361 GGLSTWMSIQGCVAPQSSFLNHTROIGTIFSAEREKRDVQPASQHEGGGAEGLSTWGV 420
QY 421 GLALAPALMWGVVCPSC 437
DB 421 GLALAPALMWGVVCPSC 437

RESULT 6
AAB65260
ID AAB65260 standard; protein; 437 AA.
AC AAB65260;
XX
XX 02-APR-2001 (first entry)
XX
XX Human PRO1181 (UNQ595) protein sequence SEQ ID NO:355.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX
XX Homo sapiens.
XX
XX WO200073454-A1.
XX

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PD 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037F.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI; 2001-032160/04.
XX N-PSDB; AAF44229.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 12; Fig 250; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX AAB65300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention
XX
XX Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVLLALLGLFTPLPGVQALLCQFGTVQHVWVKVSDLPROWTPKNTSCDSGLGCQDTLM 60
DB 1 MSVLLALLGLFTPLPGVQALLCQFGTVQHVWVKVSDLPROWTPKNTSCDSGLGCQDTLM 60
QY 61 LTESGPQSVLSLKGCTEAKDQPRVTEHRMGPLSLISYTFVCROEDFCNNLVNSLPLW 120

```

Db 61 LIESGQVSLVLSKGTCEAKDQEPVTEHRMGPCLSLISYTFVCRQEDFCNNLNSLPLW 120  
QY 121 APOPPADPGSLRCPVCLSMGCLGTTTETCPKGTTHCYDGLLRGGGIFSNLRVQGM 180  
Db 121 APOPPADPGSLRCPVCLSMGCLGTTTETCPKGTTHCYDGLLRGGGIFSNLRVQGM 180  
QY 181 PQPCNLLNGTQIEIGPVGMTENCNRKDFLCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
Db 181 PQPCNLLNGTQIEIGPVGMTENCNRKDFLCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
QY 241 GOVCQETLLIDVGLTSTLVGTGKSTVGAQNSQKTIHSAAPPGLVASYTHFCSSDLN 300  
Db 241 GOVCQETLLIDVGLTSTLVGTGKSTVGAQNSQKTIHSAAPPGLVASYTHFCSSDLN 300  
QY 301 SASSSSVLLNSLPQAPVPGDRQCPVCLGTCSSGSRMTCPRGATHCYDGYIHLG 360  
Db 301 SASSSSVLLNSLPQAPVPGDRQCPVCLGTCSSGSRMTCPRGATHCYDGYIHLG 360  
QY 361 GGLSTKMSIQGCAQPSFLLNHTQIGIFSAREKRDVQPPASQHEGGGAGLESITWGV 420  
Db 361 GGLSTKMSIQGCAQPSFLLNHTQIGIFSAREKRDVQPPASQHEGGGAGLESITWGV 420  
QY 421 GLALAPALMWGVVCPSC 437  
Db 421 GLALAPALMWGVVCPSC 437

RESULT 7

AAU83672

ID AAU83672 standard; protein; 437 AA.

XX AAU83672;

XX 08-MAY-2002 (first entry)

XX Human PRO protein, Seq ID No 162.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha.

XX Homo sapiens.

XX W0200208288-A2.

XX 31-JAN-2002.

XX 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220585P.

XX 25-JUL-2000; 2000US-0220605P.

XX 25-JUL-2000; 2000US-0220607P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220638P.

XX 25-JUL-2000; 2000US-0220664P.

XX 25-JUL-2000; 2000US-0220666P.

XX 25-JUL-2000; 2000US-0220893P.

XX 28-JUL-2000; 2000WO-US020710.

XX 01-AUG-2000; 2000US-0222425P.

XX 22-AUG-2000; 2000US-0227133P.

XX 23-AUG-2000; 2000WO-US023522.

XX 10-NOV-2000; 2000WO-US030873.

XX 28-NOV-2000; 2000US-0253646P.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 28-FEB-2001; 2000WO-US034956.

XX 01-MAR-2001; 2001WO-US0006520.

XX 22-MAR-2001; 2001US-00816744.

XX 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.  
XX 25-MAY-2001; 2001WO-US017092.  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
XX WPI; 2002-172001/22.  
DR N-PSDB; ABK3616.  
XX

One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumors such  
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor  
PT or liver tumor.

XX Claim 11; Fig 162; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumors, especially lung  
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
CC liver tumor. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
CC protein sequences of the invention  
XX

XX Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 5; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.1e-172;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSALLLALLGFIPLPGVQALLCQFCTQVHVWVKVSDLPQWTPKNTSCDSGLGQDTLM 60  
Db 1 MSALLLALLGFIPLPGVQALLCQFCTQVHVWVKVSDLPQWTPKNTSCDSGLGQDTLM 60  
QY 61 LIESGQVSLVLSKGTCEAKDQEPVTEHRMGPCLSLISYTFVCRQEDFCNNLNSLPLW 120  
Db 61 LIESGQVSLVLSKGTCEAKDQEPVTEHRMGPCLSLISYTFVCRQEDFCNNLNSLPLW 120  
QY 121 APOPPADPGSLRCPVCLSMGCLGTTTETCPKGTTHCYDGLLRGGGIFSNLRVQGM 180  
Db 121 APOPPADPGSLRCPVCLSMGCLGTTTETCPKGTTHCYDGLLRGGGIFSNLRVQGM 180  
QY 181 PQPCNLLNGTQIEIGPVGMTENCNRKDFLCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
Db 181 PQPCNLLNGTQIEIGPVGMTENCNRKDFLCHRGTTIMTHGNLAQEPDWTTSNTECEV 240  
QY 241 GOVCQETLLIDVGLTSTLVGTGKSTVGAQNSQKTIHSAAPPGLVASYTHFCSSDLN 300  
Db 241 GOVCQETLLIDVGLTSTLVGTGKSTVGAQNSQKTIHSAAPPGLVASYTHFCSSDLN 300  
QY 301 SASSSSVLLNSLPQAPVPGDRQCPVCLGTCSSGSRMTCPRGATHCYDGYIHLG 360  
Db 301 SASSSSVLLNSLPQAPVPGDRQCPVCLGTCSSGSRMTCPRGATHCYDGYIHLG 360  
QY 361 GGLSTKMSIQGCAQPSFLLNHTQIGIFSAREKRDVQPPASQHEGGGAGLESITWGV 420  
Db 361 GGLSTKMSIQGCAQPSFLLNHTQIGIFSAREKRDVQPPASQHEGGGAGLESITWGV 420  
QY 421 GLALAPALMWGVVCPSC 437  
Db 421 GLALAPALMWGVVCPSC 437

```
RESULT 8
ABG92707
ID ABG92707 standard; protein; 437 AA.
XX
AC ABG92707;
XX
DT 18-NOV-2002 (first entry)
XX
DE Human secreted protein PRO1863.
XX
KW Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW inflammatory disorder; immune related disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW psoriasis; allergic disease of the lung; graft-versus host disease;
KW tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002098506-A1.
XX
PD 25-JUL-2002.
XX
PF 27-DEC-2001; 2001US-00033301.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170362P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein D, Desnovers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2002-690475/74.
DR N-PSDB; ABS68390.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides useful
PT for diagnosis and treatment of inflammatory disorders and immune-related
PT diseases, and identifying modulators.
XX
XX Claim 12; Fig 10; 125pp; English.
XX
XX The invention relates to an isolated polypeptide having at least 80%
CC amino acid sequence identity to secreted and transmembrane polypeptides
CC PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC cells and antibodies against PRO polypeptides. PRO proteins are useful
CC for identifying modulators of the polypeptide. PRO1868 useful for the
```

```
CC diagnosis and treatment of inflammatory and immune related diseases
CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC versus host disease and tumours. Pro nucleic acids are useful for
CC constructing hybridisation probes for mapping the gene that encodes that
CC PRO and for the genetic analysis of individuals with genetic disorders,
CC and for generating transgenic animals which are useful in the development
CC and screening of therapeutically useful reagents. PRO nucleic acids are
CC also useful for gene therapy, chromosome identification, and tissue
CC typing. PRO proteins are useful as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies are useful in
CC diagnostic assays for PRO, e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO. The present
CC sequence represents a PRO protein
XX
SQ Sequence 437 AA;
Query Match 100.0%; Score 2381; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAVLLALLGFIPLPGVQALLCGFTVQHVWKVSDLPROMTPKNTSCDSGLGCQDTLM 60
DB 1 MSAVLLALLGFIPLPGVQALLCGFTVQHVWKVSDLPROMTPKNTSCDSGLGCQDTLM 60
QY 61 LIESGPQVSLVLSKGTCAKQDEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120
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QY 121 APQPPADPGSLRCPVCLSMEGCLEGTTBEICPKGTHTCYDGLLRGGGIFSNLRVQGC 180
DB 121 APQPPADPGSLRCPVCLSMEGCLEGTTBEICPKGTHTCYDGLLRGGGIFSNLRVQGC 180
QY 181 PPGCNLLNGTOEIGPVGMTENCNKDFLTCHRGTTIMTHGNLAQEPDWTTSNTMCEV 240
DB 181 PPGCNLLNGTOEIGPVGMTENCNKDFLTCHRGTTIMTHGNLAQEPDWTTSNTMCEV 240
QY 241 GQVCQETLLLDVGLTSLVGTGKSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL 300
DB 241 GQVCQETLLLDVGLTSLVGTGKSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL 300
QY 301 SASSSSVLNLSLPPQAAAPVPGDRQCPCTVQPLGTCSSGSPRMTCPRGATHCYDGYI 360
DB 301 SASSSSVLNLSLPPQAAAPVPGDRQCPCTVQPLGTCSSGSPRMTCPRGATHCYDGYI 360
QY 361 GGLSTKMSIQGCVAPQSSFLNHTROIIGIFSAREKRDVOPPASQHEGGGAEGLSLTW 420
DB 361 GGLSTKMSIQGCVAPQSSFLNHTROIIGIFSAREKRDVOPPASQHEGGGAEGLSLTW 420
QY 421 GLALAPALWGVVCPSC 437
DB 421 GLALAPALWGVVCPSC 437
RESULT 9
ABG91359
ID ABG91359 standard; protein; 437 AA.
XX
AC ABG91359;
XX
DT 29-NOV-2002 (first entry)
XX
DE Novel human secreted protein #5.
XX
KW Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW immunogenic.
XX
OS Homo sapiens.
XX
PN US2002098505-A1.
XX
PD 25-JUL-2002.
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	XX	28-DEC-2001; 2001US-00033246.	
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	PR	04-AUG-1998;	98US-0095325P.
	PR	16-DEC-1998;	98US-0112851P.
	PR	16-DEC-1998;	98US-0113145P.
	PR	22-DEC-1998;	98US-0113511P.
	PR	12-JAN-1999;	99US-0115558P.
	PR	12-JAN-1999;	99US-0115565P.
	PR	12-JAN-1999;	99US-0115733P.
	PR	09-FEB-1999;	99US-0119341P.
	PR	10-FEB-1999;	99US-0119537P.
	PR	12-FEB-1999;	99US-0119965P.
	PR	02-JUN-1999;	99WO-US01225Z.
	PR	23-OCT-1999;	99US-0162506P.
	PR	01-DEC-1999;	99WO-US028634.
	PR	02-DEC-1999;	99WO-US028551.
	PR	09-DEC-1999;	99US-0170262P.
	PR	11-FEB-2000;	2000WO-US00356S.
	PR	22-FEB-2000;	2000WO-US004414.
	PR	03-MAR-2000;	2000WO-US005841.
	PR	30-MAR-2000;	2000WO-US008439.
	PR	30-MAY-2000;	2000WO-US014941.
	PR	02-JUN-2000;	2000WO-US015264.
	PR	01-DEC-2000;	2000WO-US032678.
	PR	25-MAY-2001;	2001US-00866034.
	XX	(GETH ) GENENTECH INC.	
	XX		
	PI	Botstein D; Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A; Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Wood WI;	
	PI	WPI; 2002-665999/71. N-PSDB; ABS67458.	
	DR	New human secreted and transmembrane (PRO) polypeptides, useful for treating conditions requiring PRO polypeptides, for screening PRO antagonists and agonists useful as drug candidates.	
	PT	Claim 12; Fig 10; 125pp; English.	
	XX	The invention relates to new human secreted and transmembrane proteins (PRO) and nucleic acids of the invention. The polypeptides can be administered therapeutically, especially by expressing encoding polynucleotides, e.g. in therapeutic compositions. They can be used to screen for PRO polypeptide antagonists and agonists useful to identify drug candidates. They can also be used to produce antibodies, useful to detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or therapeutically (e.g. as antagonists or to target and/or deliver cytotoxic agents). The polynucleotides are useful therapeutically e.g. to produce antisense sequences to inhibit polypeptide production. They can be used to produce probes and primers useful to detect or isolate sequences encoding PRO polypeptides or similar sequences e.g. variants or sequences from other species. They are also useful for gene mapping and to generate transgenic animals. ABG91355-ABG91363 represent human PRO amino acid sequences of the invention	
	XX	Sequence 437 AA;	
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	Query Match	100.0%; Score 2381; DB 5; Length 437;	
	Best Local Similarity	100.0%; Pred. No. 4.1e-172;	
	Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
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	Db	 1 MSALLIALGLFILPLFGVQLLCQFTGVQHVKVSDDLPRWTPKNTSCDSELGCODTILM 60	
	QY	61 LIISGPVSLVLKSGTEAKDKQEPRTVEHRMGPGLLIYSYTVFCRQEDPCNNLNSLPIM 120	
	Db	 61 LIISGPVSLVLKSGTEAKDKQEPRTVEHRMGPGLLIYSYTVFCRQEDPCNNLNSLPIM 120	

FT /label= Transmembrane\_domain  
 FT 254..259  
 FT /note= "N-myristoylation site"  
 FT 261..266  
 FT /note= "N-myristoylation site"  
 FT 269..274  
 FT /note= "N-myristoylation site"  
 FT 284..289  
 FT /note= "N-myristoylation site"  
 FT 333..338  
 FT /note= "N-myristoylation site"  
 FT 347..352  
 FT /note= "N-myristoylation site"  
 FT 359..362  
 FT /note= "Glycosaminoglycan attachment site"  
 FT 360..365  
 FT /note= "N-myristoylation site"  
 FT 361..366  
 FT /note= "N-myristoylation site"  
 FT 382..385  
 FT /note= "N-glycosylation site"  
 FT 388..393  
 FT /note= "N-myristoylation site"  
 FT 408..413  
 FT /note= "N-myristoylation site"  
 FT 419..424  
 FT /note= "N-myristoylation site"  
 FT  
 PN US2002098507-A1.  
 XX  
 PD 25-JUL-2002.  
 XX  
 XX 27-DEC-2001; 2001US-00033326.  
 XX  
 PR 04-AUG-1998; 98US-0095325P.  
 PR 16-DEC-1998; 98US-0112851P.  
 PR 16-DEC-1998; 98US-0113145P.  
 PR 22-DEC-1998; 98US-0113511P.  
 PR 12-JAN-1999; 99US-0115558P.  
 PR 12-JAN-1999; 99US-0115565P.  
 PR 12-JAN-1999; 99US-0115733P.  
 PR 09-FEB-1999; 99US-0119341P.  
 PR 10-FEB-1999; 99US-0119537P.  
 PR 12-FEB-1999; 99US-0119965P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 01-DEC-1999; 99WO-US028551.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 25-MAY-2001; 2001US-00866034.  
 XX  
 (GETH ) GENENTECH INC.  
 XX  
 XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;  
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 DR WPI; 2002-673823/72.  
 DR N-PSDB; ABS53475.  
 XX  
 XX Novel PRO polypeptides and nucleic acids encoding the polypeptides,  
 PT useful for preparing a medicament for the treatment of inflammatory and  
 PT immune related disorders.  
 XX  
 PS Claim 12; Fig 10; 125pp; English.

XX The present invention relates to the isolation of novel human secreted  
 CC and transmembrane polypeptides, designated PRO polypeptides, and the  
 CC polynucleotide sequences encoding them. The PRO polypeptides, and the  
 CC invention include PRO1800, PRO339, PRO982, PRO1434, PRO1863, PRO1917,  
 CC PRO1868, PRO3434 and PRO1927. The PRO polypeptides can inhibit the  
 CC stimulation of T-lymphocyte proliferation. The PRO polypeptides are  
 CC useful for the diagnosis and treatment of inflammatory diseases (e.g.  
 CC inflammatory bowel disease, rheumatoid arthritis, Sjogren's syndrome,  
 CC autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus, multiple  
 CC sclerosis, hepatitis, contact dermatitis, allergic diseases and  
 CC psoriasis), immune related diseases, and kidney diseases in humans. The  
 CC present sequence represents human PRO1863 polypeptide  
 XX  
 SQ Sequence 437 AA;  
 Query Match 100.0%; Score 2381; DB 5; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 4.le-172;  
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSAVLLALLGLFILPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDTLM 60  
 Db 1 MSAVLLALLGLFILPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDGLGCDTLM 60  
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 Db 61 LIESGPQVSLVSKGCTEAKDQEPVTEHRMGPGLSLISYTFVCROEDFCNNLVNSLPLW 120  
 QY 121 AFQPPADPGSLRCPVCLSMEGCLEGTTEICPKGTHCYDGLLRGGGIFSNLRVQGC 180  
 Db 121 AFQPPADPGSLRCPVCLSMEGCLEGTTEICPKGTHCYDGLLRGGGIFSNLRVQGC 180  
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 Db 181 POPGNNLNGTOEIGVPVGMTECNCRKDFLTCHRGTTIMTHGNLAQPTDWTNTENCEV 240  
 QY 241 GQVCQETLLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGLVAVSYTHFCSSDLN 300  
 Db 241 GQVCQETLLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGLVAVSYTHFCSSDLN 300  
 QY 301 SASSSVLLNSLPPQAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
 Db 301 SASSSVLLNSLPPQAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
 QY 361 GGLSTKMSIQGCVAPQSPFLLNHTROIIGIFSAREKRDVOPPASQHEGGGAGLESITWGV 420  
 Db 361 GGLSTKMSIQGCVAPQSPFLLNHTROIIGIFSAREKRDVOPPASQHEGGGAGLESITWGV 420  
 QY 421 GLALAPALMWGVVCPSC 437  
 Db 421 GLALAPALMWGVVCPSC 437  
 RESULT 11  
 ADY31902  
 ID ADY31902 standard; protein; 437 AA.  
 XX  
 AC ADY31902;  
 XX  
 XX 05-MAY-2005 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO1181.  
 XX  
 KW PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer;  
 KW lung; colon; breast; prostate; rectum; liver;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;  
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;  
 KW arthritis; sports injury; cytostatic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200193983-A1.  
 XX

13-DEC-2001.  
XX PF 01-JUN-2001; 2001WO-US017800.  
XX 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 20-JUN-2000; 2000US-0212901P.  
PR 22-JUN-2000; 2000US-0213807P.  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220585P.  
PR 25-JUL-2000; 2000US-0220605P.  
PR 25-JUL-2000; 2000US-0220607P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220638P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 25-JUL-2000; 2000US-0220666P.  
PR 26-JUL-2000; 2000US-0220893P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-AUG-2000; 2000US-0222425P.  
PR 22-AUG-2000; 2000US-0227133P.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 28-NOV-2000; 2000US-0253646P.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 25-MAY-2001; 2001WO-US017092.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CX, Wood WT;  
XX WPI; 2002-404358/43.  
DR N-ESDB; ADY31901.  
XX  
PT Isolated nucleic acid useful in a method for stimulating the  
PT proliferation, gene expression or differentiation of cells and in  
PT detecting the presence of a tumor.  
XX  
XX Claim 11; SEQ ID NO 162; 296bp; English.  
XX  
XX The invention relates to human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.  
CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. They are particularly useful for  
CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,  
CC prostate tumour, rectal tumour or liver tumour) in a mammal, for  
CC stimulating the release of tumour necrosis factor (TNF)-alpha from human  
CC blood, for stimulating the proliferation or differentiation of  
CC chondrocyte cells, for stimulating the proliferation of or gene  
CC expression in pericyte cells or for stimulating the proliferation of  
CC normal human dermal fibroblasts. The PRO nucleic acids are useful as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant  
CC technology, in generating transgenic animals or knock-out animals which  
CC may be used in the development and screening of therapeutically useful  
CC reagents, in gene therapy, in chromosome identification, as chromosome  
CC markers and in generating probes. The PRO polypeptides, or anti-PRO  
CC antibodies, are useful for preparing a medicament for treating a  
CC condition which is responsive to the PRO polypeptides or anti-PRO  
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage  
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-  
CC differentiation of chondrocytes. The PRO polypeptides are useful as  
CC molecular markers for protein electrophoresis, and in tissue typing. This  
CC sequence represents a human PRO polypeptide of the invention. Note: The  
CC sequence data for this patent is also available in electronic format from

CC USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 437 AA;  
Query Match 100.0%; Score 2381; DB 5; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4,1e-172;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MSVALLALLGLFILPLGVQALLCQFGTVQHVWVSDLPROWTPKNTSCDGLGCGQDTLM 60  
QY 61 LIESGPQVSLVSKGCTEAKDQEPRTVEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120  
DB 61 LIESGPQVSLVSKGCTEAKDQEPRTVEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120  
QY 121 APQPPADPGSLRCPVCLSMEGCLEGTTEICPKGTTTCYDGLLRGGGIFSNLRVQCGM 180  
DB 121 APQPPADPGSLRCPVCLSMEGCLEGTTEICPKGTTTCYDGLLRGGGIFSNLRVQCGM 180  
QY 181 PQGCNLLNGTOEIGPVGMTENCNRKDFLTCHRGTTTMTGNLAQEPDWTTSNTEMCV 240  
DB 181 PQGCNLLNGTOEIGPVGMTENCNRKDFLTCHRGTTTMTGNLAQEPDWTTSNTEMCV 240  
QY 241 GQVQETLLLDVGLTSLVGTGKSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL 300  
DB 241 GQVQETLLLDVGLTSLVGTGKSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL 300  
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DB 301 SASSSVLLNSLPPQAAAPVPGDRQCPVQLGTCSSGSPRMTCPRGATHCYDGYIHLSG 360  
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DB 361 GGLSTKMSIOGCVAPQSSFLNHTROJGIFSAERKRDVQPPASOHEGGGAGLSLTWGV 420  
QY 421 GLALAPALWGWVCPSC 437  
DB 421 GLALAPALWGWVCPSC 437  
RESULT 12  
ABU72375  
ID ABU72375 standard; protein; 437 AA.  
XX  
AC ABU72375;  
XX  
DT 16-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO1863.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytostatic;  
KW antiinflammatory; dermatological; immunosuppressive; antirheumatic;  
KW antithyroid; haemostatic; antithyroid; neuroprotective; hepatotropic;  
KW viricide; antiproliferative; antiallergic; gene therapy; colon cancer;  
KW inflammatory bowel disease; systemic lupus erythematosus; hepatitis;  
KW rheumatoid arthritis; scleroderma; Sjogren's syndrome; thyroiditis;  
KW thrombocytopaenia; multiple sclerosis; cystic fibrosis; psoriasis;  
KW allergy; graft-versus-host disease; graft rejection.  
XX Homo sapiens.  
XX  
FN US2002182618-A1.  
XX  
XX 05-DEC-2002.  
XX  
XX 27-DEC-2001; 2001US-00033167.  
XX  
XX 04-AUG-1998; 98US-0095325P.  
PR 16-DEC-1998; 98US-0112851P.  
PR 16-DEC-1998; 98US-0113145P.  
PR 22-DEC-1998; 98US-0113511P.  
PR 12-JAN-1999; 99US-0115558P.

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PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119377P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US011252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-FEB-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
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PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
XX WPI; 2003-328610/31.
DR N-PSDB; ACA64082.
XX
XX New secreted and transmembrane PRO polypeptides or genes encoding them,
PT useful for treating e.g. colon cancer, inflammatory bowel disease,
PT Sjogren's syndrome, thrombocytopenia, thyroiditis, multiple sclerosis or
PT graft rejection.
XX
XX Claim 12; Fig 10; 119pp; English.
XX
XX The invention describes an isolated secreted and transmembrane
CC polypeptide (PRO), which scores at least 80% amino acid sequence identity
CC when compared to: (a) a sequence comprising 278, 830, 125, 325, 437, 487,
CC 310, 1029 or 548 amino acids fully defined in the specification; (b) any
CC of the sequences of (a), lacking its associated signal peptide; (c) an
CC extracellular domain of (a), with or lacking its associated signal
CC peptide. The PRO polypeptide or polynucleotide is useful as
CC pharmaceuticals or diagnostics. These are particularly useful for
CC treating colon cancer, inflammatory bowel disease, systemic lupus
CC erythematosus, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC thrombocytopenia, thyroiditis, multiple sclerosis, hepatitis, cystic
CC fibrosis, psoriasis, allergies, graft-versus-host disease or graft
CC rejection in a mammal. This is the amino acid sequence of a novel human
CC secreted and transmembrane PRO polypeptide
XX
XX Sequence 437 AA;
SQ
Query Match 100.0%; Score 2381; DB 6; Length 437;
Best Local Similarity 100.0%; Pred. NO. 4.1e-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSAVLLIALLGFTLPLPGVALLCGFTGVHVKVSDLPQWTPKNTSCDSGLGCCDTLM 60
DB 1 MSAVLLIALLGFTLPLPGVALLCGFTGVHVKVSDLPQWTPKNTSCDSGLGCCDTLM 60
QY 61 LIESGQVSVLVSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
DB 61 LIESGQVSVLVSKGCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLW 120
QY 121 APQPPADPSGLRCPVCLSMGCLGTTTCEI CPKGTTHCYDGLLRGGGIFSNLRVQGM 180
DB 121 APQPPADPSGLRCPVCLSMGCLGTTTCEI CPKGTTHCYDGLLRGGGIFSNLRVQGM 180
QY 181 PQGECNLLNGTOEIGPVGMTENCNRKDFLCHRTTLMTHGNLAQEPDWTNTENCEV 240
DB 181 PQGECNLLNGTOEIGPVGMTENCNRKDFLCHRTTLMTHGNLAQEPDWTNTENCEV 240

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QY 241 GQVCQETLLLDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPGVILVASYTHFCSSDLCN 300
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QY 301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360
DB 301 SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360
QY 361 GGLSTKMSIQGCAQPSFLLNHTROI GIFSAREKRDVQPPASQHEGGGAGLESITWGV 420
DB 361 GGLSTKMSIQGCAQPSFLLNHTROI GIFSAREKRDVQPPASQHEGGGAGLESITWGV 420
QY 421 GLALAPALWGVVCPSC 437
DB 421 GLALAPALWGVVCPSC 437
RESULT 13
ABUS8075
ID ABUS8075 standard; protein; 437 AA.
XX
AC ABUS8075;
XX
XX 14-APR-2003 (first entry)
XX
XX Human PRO polypeptide #107.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
XX
XX US2003027163-A1.
XX
XX 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
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XX 09-JUN-1998; 98US-0088655P.
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 PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumaas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-247083/24.  
 DR N-PSDB; ABX80352.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments.  
 XX  
 PS Claim 12; Fig 250; 648pp; English.

CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO826, PRO826, PRO1068 or PRO132 enhance survival of  
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and are  
 CC thus useful for treating sports injuries, and arthritis. This is the  
 CC amino acid sequence of a novel human PRO protein

XX Sequence 437 AA;

Query Match 100.0%; Score 2381; DB 6; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-172;  
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 Qy 421 GLALAPALMWGVVCPSC 437  
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 Db 421 GLALAPALMWGVVCPSC 437  
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 ABU80865  
 ID ABU80865 standard; protein; 437 AA.  
 XX  
 AC ABU80865;  
 XX  
 DT 23-JUN-2003 (first entry)  
 XX  
 DE Human secreted and transmembrane polypeptide PRO1863.  
 XX  
 KW Human; gene therapy; inflammatory disease; Crohn's disease;  
 KW inflammatory bowel disease; ulcerative colitis; tumour; cancer;  
 KW colorectal cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002192668-A1.  
 XX  
 PD 19-DEC-2002.  
 XX  
 PF 27-DEC-2001; 2001US-00033244.  
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XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AU, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
XX WPI; 2003-328857/31.
DR N-PSDB; ACA66975.
DR
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammatory diseases, tumors or cancer.
XX
XX Claim 12; Fig 10; 119pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases such as inflammatory bowel disease, ulcerative
CC colitis and Crohn's disease, tumors, or cancer such as colorectal
CC cancer. The nucleic acids are useful as hybridisation probes, in
CC chromosome and gene mapping and in generating antisense RNA or DNA. The
CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. Both are useful in tissue typing. The present sequence
CC represents the amino acid sequence of a PRO polypeptide of the invention
XX
XX Sequence 437 AA;
SQ
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Best Local Similarity 100.0%; Pred. No. 4.le-172;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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Db 421 GLALAPALMWGVCPSC 437

## RESULT 2

US-989-723-355  
Sequence 355, Application US/09989723  
Patent No. US20020072092A1

## GENERAL INFORMATION:

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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730PIC62  
;; CURRENT APPLICATION NUMBER: US/09/989,723  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
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/ PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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APPLICANT: Desnoyers, Luc  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
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TITLE OF INVENTION: Acids Encoding the Same  
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; APPLICANT: Zhang, Zemin
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140 ; PRIOR FILING DATE: 1998-07-07  
141 ; PRIOR APPLICATION NUMBER: 60/092182  
142 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;  
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Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LIESGPOVSLVLSKGTCTAKQDEPRVTEHRMGPGLSLSYTFVCRQEDFCNNLVNSLPW 120  
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Db 121 APQPPADPGSRCPVCLSMCEGTEGTTEEI CPKGTTHCYDGLRLRGGGIFSNLRVQGM 180  
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Db 181 POPCNLLNGTQETGPVCMTCNCRKDFLTCHRGTTIMTHNLAQEPDWTTSNTECEV 240  
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Qy 421 GLALAPALWGWVCPSC 437  
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; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC70  
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-09  
  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.

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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1G57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;

Best Local Similarity 100.0%; Pred. No. 4.7e-194;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LIESGPQVSLVLSKGTEAKDQEPVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120  
Qy 121 APQPPADPGSLRCPVLSMEGLSGTTEECIPKGTTHCYDGLLRGGGIFSNLRVQCM 180  
Db 121 APQPPADPGSLRCPVLSMEGLSGTTEECIPKGTTHCYDGLLRGGGIFSNLRVQCM 180  
Qy 181 POPCNLLNGTOEIGPVGMTENCRKDFLTCHRGCTTMTNLAQEPDWTTSNTCEV 240  
Db 181 POPCNLLNGTOEIGPVGMTENCRKDFLTCHRGCTTMTNLAQEPDWTTSNTCEV 240  
Qy 241 GOVCQETLLLDVGLTSTLVGTGKCVTGAQNSOKTTHSAPPGVLVASYTHFCSDDL 300  
Db 241 GOVCQETLLLDVGLTSTLVGTGKCVTGAQNSOKTTHSAPPGVLVASYTHFCSDDL 300  
Qy 301 SASSSVLLNSLPQAAAPVPGDRQCPTCVPLGTCSGSPRMTCPRGATHCYDGYIHL 360  
Db 301 SASSSVLLNSLPQAAAPVPGDRQCPTCVPLGTCSGSPRMTCPRGATHCYDGYIHL 360  
Qy 361 GGLSTKMSIQCVAPQPSFLNHTHQIGFSAAREKRDVQPASQHEGGAGLESLSL 420  
Db 361 GGLSTKMSIQCVAPQPSFLNHTHQIGFSAAREKRDVQPASQHEGGAGLESLSL 420  
Qy 421 GLALAPALWGVVCPSC 437  
Db 421 GLALAPALWGVVCPSC 437

Db 421 GLALAPALWGVVCPSC 437

RESULT 7

US-09-991-073-355  
; Sequence 355, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730FIC15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.7e-194;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 GLALAPALWGVVCPSC 437

RESULT 8

US-09-990-442-355  
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; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322

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; PRIOR FILING DATE: 1998-06-17  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991.163  
PRIOR FILING DATE: 2001-11-14  
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;/ PRIOR APPLICATION NUMBER: 60/091982  
;/ PRIOR FILING DATE: 1998-07-07  
;/ PRIOR APPLICATION NUMBER: 60/092182  
;/ PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2381; DB 3; Length 437;

Best Local Similarity 100.0%; Pred. No. 4.7e-194;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LIESGQVSLVLSKGTCEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSIPLW 120  
QY 121 APOPPADPSLRCPVCLSMGCLLEGTTTEICPKGTHCYDGLRLRGGGIFSNLRVQGM 180  
DB 121 APOPPADPSLRCPVCLSMGCLLEGTTTEICPKGTHCYDGLRLRGGGIFSNLRVQGM 180  
QY 181 PQGCNLLNCTQRIQPGVMTENCNRKDFLTCRGTITMTGNLAQEPDWTNTNTECEV 240  
DB 181 PQGCNLLNCTQRIQPGVMTENCNRKDFLTCRGTITMTGNLAQEPDWTNTNTECEV 240  
QY 241 GOVCQETLLLDVGLTSLVTGTCSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLN 300  
DB 241 GOVCQETLLLDVGLTSLVTGTCSTVGAQNSOKTTIHSAPPGVLVASYTHFCSSDLN 300  
QY 301 SASSSSVLLNSLPQAAVPDGRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
DB 301 SASSSSVLLNSLPQAAVPDGRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
QY 361 GGLSTRKMSIOGCVQAQPSFLNHTQIGTIFSAKRDVQPPASQHEGGAGLESITWGV 420  
DB 361 GGLSTRKMSIOGCVQAQPSFLNHTQIGTIFSAKRDVQPPASQHEGGAGLESITWGV 420  
QY 421 GLALAPALMWGVCPSC 437  
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RESULT 10

US-09-993-604-355  
; Sequence 355, Application US/09993604  
; Patent No. US20020137075A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

;/ APPLICANT: Botstein, David  
;/ APPLICANT: Desnoyers, Luc  
;/ APPLICANT: Eaton, Dan L.  
;/ APPLICANT: Ferrara, Napoleone  
;/ APPLICANT: Fong, Sherman  
;/ APPLICANT: Gerber, Hanspeter  
;/ APPLICANT: Gerritsen, Mary E.  
;/ APPLICANT: Goddard, Audrey  
;/ APPLICANT: Godowski, Paul J.  
;/ APPLICANT: Grimaldi, J. Christopher  
;/ APPLICANT: Gurney, Austin L.  
;/ APPLICANT: Kljavin, Ivar J.  
;/ APPLICANT: Napier, Mary A.  
;/ APPLICANT: Pan, James  
;/ APPLICANT: Paoni, Nicholas F.  
;/ APPLICANT: Roy, Margaret Ann  
;/ APPLICANT: Stewart, Timothy A.  
;/ APPLICANT: Tumas, Daniel  
;/ APPLICANT: Watanabe, Colin K.  
;/ APPLICANT: Williams, P. Mickey  
;/ APPLICANT: Wood, William I.  
;/ APPLICANT: Zhang, Zemin  
;/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;/ FILE REFERENCE: P2730PIC25  
;/ CURRENT APPLICATION NUMBER: US/09/993,604  
;/ CURRENT FILING DATE: 2001-11-14  
;/ PRIOR APPLICATION NUMBER: 60/049787  
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Qy	121	APQPPADPGSLRCPVCLSMEGCLEGTTTEECPKGTTHCYDGLLRGGGIFSNLRVQCGM	180
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Qy	181	PQPCNLLNGTQEIIGPVGMTECNCRKDFLTCHRGTTTMTGNLAQEPDWTTSNTECEV	240
Db	181	PQPCNLLNGTQEIIGPVGMTECNCRKDFLTCHRGTTTMTGNLAQEPDWTTSNTECEV	240
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;; PRIOR FILING DATE: 1998-07-07  
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Query Match 100.0%; Score 2381; DB 3; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.7e-194;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 LIESGPQVSLVLSKGTCTEAKDQEPRTVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW 120  
Qy 121 APOPPADPGSLRCPVCLSMCECLGTTTBEICPKGTHTCYDGLLRGGGIFSNLRVQCGM 180  
Db 121 APOPPADPGSLRCPVCLSMCECLGTTTBEICPKGTHTCYDGLLRGGGIFSNLRVQCGM 180  
Qy 181 POPCNLLNGTOEIGPVGMTENCNKRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTEMCEV 240  
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Qy 241 GQVCQETLLLDVGLTSTLVGTGKSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLN 300  
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Db 301 SASSSSVLLNSLPPQAAAPVPGDRQCPTCVQPLGTCCSSSPRMTCPRGATHCYDGYIHLSG 360  
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Qy 421 GLALAPALMWGVVCPSC 437  
Db 421 GLALAPALMWGVVCPSC 437

## RESULT 12

US-09-989-721-355  
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; Patent No. US20020142961A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C55  
; CURRENT APPLICATION NUMBER: US/09/989,721  
; CURRENT FILING DATE: 2001-11-19  
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,	PRIOR FILING DATE:	1998-06-12
,	PRIOR APPLICATION NUMBER:	60/089440
,	PRIOR FILING DATE:	1998-06-16
,	PRIOR APPLICATION NUMBER:	60/089512



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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LIESGPQSVLSVLSKGCTEAKDQEPVTEHRMGPGLSLSIYTFVCRQDFCNLNSPLW 120
Db 61 LIESGPQSVLSVLSKGCTEAKDQEPVTEHRMGPGLSLSIYTFVCRQDFCNLNSPLW 120

QY 121 APOPPADPGSLRCPVCLSMGCLGTTETEEICPKGTHCYDGLRLRGGIFSNLRVQGM 180
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QY 181 PQPCNLLNGTQBIGPVGMTECNCRKDFLCHRGTTHMTHGNAQEPDWTNTSNTCEV 240
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QY 241 GQVCOETLLIDVGLTSLVGTGKCVSTVGAQNSQKTIHSAAPPQVLVASTHFCSSDLN 300
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QY 301 SASSSSVLLNSLPQAPVDPDROCPTCVPLGTCCSSGSPMTCPRGATHCYDGYIHLG 360
Db 301 SASSSSVLLNSLPQAPVDPDROCPTCVPLGTCCSSGSPMTCPRGATHCYDGYIHLG 360

QY 361 GGLSTKMSIQGCVAQPSFLNHTHQIGIFSAREKRDVQPPASQHEGGGAEGLSLTWG 420
Db 361 GGLSTKMSIQGCVAQPSFLNHTHQIGIFSAREKRDVQPPASQHEGGGAEGLSLTWG 420

QY 421 GLALAPALWGVVCPSC 437
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## RESULT 13

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US-09-992-598-355
Sequence 355, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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Db 421 GLALAPALWGVCFSC 437  
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Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS  
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CURRENT FILING DATE: 2001-11-20  
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PRIOR FILING DATE: 1997-06-16  
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55 PRIOR APPLICATION NUMBER: 60/091978  
56 PRIOR FILING DATE: 1998-07-07  
57 PRIOR APPLICATION NUMBER: 60/091982  
58 PRIOR FILING DATE: 1998-07-07  
59 PRIOR APPLICATION NUMBER: 60/092182  
60 PRIOR FILING DATE: 1998-07-09

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DB 61 LIESGQVSLVLSKGCCTEAKDQPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSPLW 120

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DB 121 APQPPADPGSLRCPVCLSMEGCLGTTBEICPKGTHCYDGLRLRGGGIFSNLRVQCGM 180  
QY 181 POPGCLNLANGTOEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTNTNTECEV 240  
DB 181 POPGCLNLANGTOEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTNTNTECEV 240  
QY 241 GOVCQETLLLDVGLTSTLVGTMGKSTVGAQNSQKTTIHSAPFGLVLSYTHFCSSDLN 300  
DB 241 GOVCQETLLLDVGLTSTLVGTMGKSTVGAQNSQKTTIHSAPFGLVLSYTHFCSSDLN 300  
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DB 301 SASSSSVLLNSLPPQAAVPVGRQCTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360  
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DB 421 GLALAPALMWGVVCPSC 437

RESULT 15  
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; Sequence 355, Application US/09989735  
; Publication No. US20020193299A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C61  
; CURRENT APPLICATION NUMBER: US/09/989,735  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

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Query Match      100.0%; Score 2381; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.7e-194; Indels 0; Gaps 0;
Matches 437; Conservative 0; Mismatches 0;

Qy      1  MSAVLLIALIGFILPLPGVQALLCQFCTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLM 60
Db      1  MSAVLLIALIGFILPLPGVQALLCQFCTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLM 60

Qy     61  LIESGQVSVLSKGTCTEAKDQBPVTEHRMGPGLSLSIYTFVCRQEDFCNNLVNSLPLW 120
Db     61  LIESGQVSVLSKGTCTEAKDQBPVTEHRMGPGLSLSIYTFVCRQEDFCNNLVNSLPLW 120

Qy    121  APOPPADPGSLRCFVCLSMEGCLEGTTTEEICPKGTTTCYDGLLRGRGGIFSNLRVQGM 180
Db    121  APOPPADPGSLRCFVCLSMEGCLEGTTTEEICPKGTTTCYDGLLRGRGGIFSNLRVQGM 180

Qy    181  PQGCNLLNGTQEIIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTMCEV 240
Db    181  PQGCNLLNGTQEIIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPDWTTSNTMCEV 240

Qy    241  GQVCQETLLLDVGLTSTLVGTGKCSVVGAGNSQKTTIHSAPPGVLVASYTHFCSSDLGN 300
Db    241  GQVCQETLLLDVGLTSTLVGTGKCSVVGAGNSQKTTIHSAPPGVLVASYTHFCSSDLGN 300

Qy    301  SASSSSVLLNSLPQAAAPVPGDROCTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360
Db    301  SASSSSVLLNSLPQAAAPVPGDROCTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG 360

Qy    361  GGLSTKMSIOGCVAPQSPSFLNHTROIIGIFSAREKRDVQPPASOHEGGGAEGLSITWGV 420
Db    361  GGLSTKMSIOGCVAPQSPSFLNHTROIIGIFSAREKRDVQPPASOHEGGGAEGLSITWGV 420

Qy    421  GLALAPALMWGVCPSC 437
Db    421  GLALAPALMWGVCPSC 437
```

Search completed: July 11, 2006, 09:34:47  
Job time : 187 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 10:29:39 ; Search time 1048 Seconds  
(without alignments)  
10644.654 Million cell updates/sec

Title: US-10-727-619-1

Perfect score: 1600

Sequence: 1 aaagcagaagagattacc.....ctgataatacacagacctgtc 1600

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 8:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

14: Geneseqn2005s:\*

15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1600	100.0	1600	3	AAA12386 Human PRV
2	1600	100.0	1600	4	Aaf61560 Human PRV
3	1599.6	100.0	1630	12	Adg21061 Human sof
4	1599.6	100.0	1630	14	Aea04409 Human cDN
5	1598.4	99.9	1692	12	Adg24979 Human sof
6	1584	99.0	1612	6	Aba97156 Human gra
7	1579.4	98.7	1587	3	Aaz65083 Membrane-
8	1579.4	98.7	1587	3	Aas51263 Human DNA
9	1579.4	98.7	1587	4	Aas21476 Human cDN
10	1579.4	98.7	1587	5	Aaf44229 Human PRO
11	1579.4	98.7	1587	6	Abk33616 cDNA enco
12	1579.4	98.7	1587	6	Abk68390 Human cDN
13	1579.4	98.7	1587	6	Abk67458 cDNA enco
14	1579.4	98.7	1587	6	Abk53475 cDNA enco
15	1579.4	98.7	1587	7	Ady31901 Novel hum
16	1579.4	98.7	1587	8	Aca64398 Novel hum
17	1579.4	98.7	1587	8	Aca03835 cDNA enco
18	1579.4	98.7	1587	8	Abx11171 cDNA enco

19	1579.4	98.7	1587	8	ABX89373	Abx89373 DNA enco
20	1579.4	98.7	1587	8	ABX80857	Abx80857 Human sec
21	1579.4	98.7	1587	8	ACD44366	ACd44366 cDNA enco
22	1579.4	98.7	1587	8	ACD42027	ACd42027 Human sec
23	1579.4	98.7	1587	8	ACA68577	ACA68577 Novel hum
24	1579.4	98.7	1587	8	ABX79537	Abx79537 Human sec
25	1579.4	98.7	1587	8	ABX90607	Abx90607 Human sec
26	1579.4	98.7	1587	8	ACA93558	ACA93558 Novel hum
27	1579.4	98.7	1587	8	ABX81240	Abx81240 Novel hum
28	1579.4	98.7	1587	8	ACA04256	ACA04256 Human cDN
29	1579.4	98.7	1587	8	ACA67365	ACA67365 cDNA enco
30	1579.4	98.7	1587	8	ACA93056	ACA93056 Novel hum
31	1579.4	98.7	1587	8	ABX17140	Abx17140 Human PRO
32	1579.4	98.7	1587	8	ACA67995	ACA67995 Novel hum
33	1579.4	98.7	1587	9	ACA88444	ACA88444 Human sec
34	1579.4	98.7	1587	9	ACD81951	ACd81951 cDNA enco
35	1579.4	98.7	1587	9	ADA45984	Ada45984 Novel hum
36	1579.4	98.7	1587	9	ADA76415	Ada76415 Human PRO
37	1579.4	98.7	1587	9	ABT44306	ABt44306 Human PRO
38	1579.4	98.7	1587	9	ADA19065	Ada19065 Human PRO
39	1579.4	98.7	1587	9	ADA61688	Ada61688 Homo sapi
40	1579.4	98.7	1587	9	ADB19473	ADB19473 Novel hum
41	1579.4	98.7	1587	9	ADB28014	ADB28014 cDNA enco
42	1579.4	98.7	1587	9	ADA86493	Ada86493 Novel hum
43	1579.4	98.7	1587	9	ADB16057	ADB16057 Human PRO
44	1579.4	98.7	1587	9	ADA37865	Ada37865 Human cDN
45	1579.4	98.7	1587	9	ADA47843	Ada47843 Human PRO

## ALIGNMENTS

### RESULT 1

AAA12386 AAA12386 standard; DNA; 1600 BP.

XX

AC AAA12386;

XX

DT 17-AUG-2000 (first entry)

XX

DE Human PRV-1 DNA.

XX

KW PRV-1; human; polycythaemia rubra vera; PRV; antiproliferative;

KW treatment; detection; diagnosis; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 36..1349

FT /\*tag= a

FT /product= "PRV-1"

XX

PN DE19849044-Al.

XX

PD 27-APR-2000.

XX

PF 23-OCT-1998; 98DE-01049044.

XX

PR 23-OCT-1998; 98DE-01049044.

XX

PA (UVFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.

XX

PI Pahl H, Ternerinac S;

XX

WPI; 2000-319347/28.

DR P-PSDB; AAY87750.

XX

PT New polycythemia rubra vera-related polypeptide useful for diagnosis and

PT for developing therapeutic antibodies.

XX

PS Claim 1; Fig 1; 6pp; German.

XX

CC This invention describes a novel PRV-1 protein (I) detected in humans



CC suffering from the condition polycythaemia rubra vera (PRV). The product  
CC of the invention has antiproliferative activity. The encoding nucleic  
CC acid sequence is used to express recombinant PRV-1 polypeptides and as a  
CC source of antisense sequences that can be expressed in vivo for treatment  
CC of PRV. (I) is used to raise specific mono or polyclonal antibodies and  
CC these are used to diagnose PRV (by detecting (I), or its epitopes, in  
CC immunoassays) or for treatment of PRV (optionally when coupled to a  
CC cytotoxin). This sequence encodes the human PRV-1 protein described in  
CC the method of the invention  
XX

SQ Sequence 1600 BP; 340 A; 490 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 100.0%; Score 1600; DB 3; Length 1600;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGCAGAAAGAGATTACAGCCACAGACGGGTCTATGACGGCGGTATTACTCTGGCCC 60  
DB 1 AAAAGCAGAAAGAGATTACAGCCACAGACGGGTCTATGACGGCGGTATTACTCTGGCCC 60  
QY 61 TCCTGGGGTTTCATCTCCCACTGCCAGGAGTGCAGGCGTCTCTGCAGTTTGGGACAG 120  
DB 61 TCCTGGGGTTTCATCTCCCACTGCCAGGAGTGCAGGCGTCTCTGCAGTTTGGGACAG 120  
QY 121 TTCAGCATGTGTGGAAAGTGTCCGACCTGCCCCGCAATGGACCCCTTAAGAACACACAGCT 180  
DB 121 TTCAGCATGTGTGGAAAGTGTCCGACCTGCCCCGCAATGGACCCCTTAAGAACACACAGCT 180  
QY 181 GCAGACGGCGTTGGGGTGCAGGACACGTTGATGCTATTGAGAGGGACCCCAAGTGA 240  
DB 181 GCAGACGGCGTTGGGGTGCAGGACACGTTGATGCTATTGAGAGGGACCCCAAGTGA 240  
QY 241 GCCTGGTGTCTCCAAAGGGTGCAGGAGGCCAAGGACAGGAGCCCGCGTCACTGAGC 300  
DB 241 GCCTGGTGTCTCCAAAGGGTGCAGGAGGCCAAGGACAGGAGCCCGCGTCACTGAGC 300  
QY 301 ACCGGATGGGCCCGCGCTCTCCCTGATCTCTACACCTTCGTGTGCGCCAGGAGACT 360  
DB 301 ACCGGATGGGCCCGCGCTCTCCCTGATCTCTACACCTTCGTGTGCGCCAGGAGACT 360  
QY 361 TCTGCAACAACTCGTTAACTCCGTCGCTTGGGGCCACAGCCGCCAGGAGCCAG 420  
DB 361 TCTGCAACAACTCGTTAACTCCGTCGCTTGGGGCCACAGCCGCCAGGAGCCAG 420  
QY 421 GATCTTTGAGTGCAGGACACACACTGTTGATGAGAGGCTCTCTGAGAGGGACAAAG 480  
DB 421 GATCTTTGAGTGCAGGACACACACTGTTGATGAGAGGCTCTCTGAGAGGGACAAAG 480  
QY 481 AGATCTGCCCAAGGGACACACACTGTTGATGAGAGGCTCTCTGAGAGGGAG 540  
DB 481 AGATCTGCCCAAGGGACACACACTGTTGATGAGAGGCTCTCTGAGAGGGAG 540  
QY 541 GCATCTTCTCAATCTGAGAGTCCAGGGATGATGCCCGCCAGCCAGGTGCAACTGCTCA 600  
DB 541 GCATCTTCTCAATCTGAGAGTCCAGGGATGATGCCCGCCAGCCAGGTGCAACTGCTCA 600  
QY 601 ATGGGACACAGGAAATTTGGGCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660  
DB 601 ATGGGACACAGGAAATTTGGGCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTC 660  
QY 661 TGACCTGTCTATCGGGGACCAACATTATGACACAGGAACTTTGGCTCAAGAACCCACTG 720  
DB 661 TGACCTGTCTATCGGGGACCAACATTATGACACAGGAACTTTGGCTCAAGAACCCACTG 720  
QY 721 ATTGGACCACTCGAATACCGAGATGTGCGAGGTGGGGAGGTGTGTCTCAGACACGCTGC 780  
DB 721 ATTGGACCACTCGAATACCGAGATGTGCGAGGTGGGGAGGTGTGTCTCAGACACGCTGC 780  
QY 781 TGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAGGCTGCAGCACTGTTG 840  
DB 781 TGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAGGCTGCAGCACTGTTG 840  
QY 841 GGGCTCAAAATTTCCAGAGACCAACCATCCACTCAGCCCTCTCTGGGGTCTTGTGGCCT 900

DB 841 GGGCTCAAAATTTCCAGAGACCAACCATCACTCAGCCCTCTCTGGGGTCTTGTGGCCT 900  
QY 901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCGTTCTGC 960  
DB 901 CCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCGTTCTGC 960  
QY 961 TGAACCTCCCTCCTCCTCAAGCTGCCCCTGTCCAGGAGACCGGCAAGTGTCTACCTGTG 1020  
DB 961 TGAACCTCCCTCCTCCTCAAGCTGCCCCTGTCCAGGAGACCGGCAAGTGTCTACCTGTG 1020  
QY 1021 TGAGAGCCCTTGGAACCTGTTCAAGTGGTCTCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080  
DB 1021 TGAGAGCCCTTGGAACCTGTTCAAGTGGTCTCCCCCGAATGACCTGCCCCAGGGGCGCCA 1080  
QY 1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGCCACCAAAATGAGCA 1140  
DB 1081 CTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGCCACCAAAATGAGCA 1140  
QY 1141 TTCAGGGCTGCGTGGCCCCAACCTTCCAGCTTCTTGTGTAACACACACAGACAAATCGGGA 1200  
DB 1141 TTCAGGGCTGCGTGGCCCCAACCTTCCAGCTTCTTGTGTAACACACACAGACAAATCGGGA 1200  
QY 1201 TCTTCTCTGCGGTGAGAAAGCGTGTGAGAGCTCTCGCTCTCAGCATGAGGAGGTG 1260  
DB 1201 TCTTCTCTGCGGTGAGAAAGCGTGTGAGAGCTCTCGCTCTCAGCATGAGGAGGTG 1260  
QY 1261 GGGCTGAGGGCTGAGAGTCTCTCAGTTGGGGGTGGGCTTGGCACTGGCCCCAGCGCTGT 1320  
DB 1261 GGGCTGAGGGCTGAGAGTCTCTCAGTTGGGGGTGGGCTTGGCACTGGCCCCAGCGCTGT 1320  
QY 1321 GGTGGGAGTGGTTTGGCCCTTCTGCTAACTCTATTACCCCCACAGATTCTTCAACCGCTGC 1380  
DB 1321 GGTGGGAGTGGTTTGGCCCTTCTGCTAACTCTATTACCCCCACAGATTCTTCAACCGCTGC 1380  
QY 1381 TGACCAACCACTCAACCTCTGACCTCATAACTTAATGGCTTGGGAGGAGGAGCT 1440  
DB 1381 TGACCAACCACTCAACCTCTGACCTCATAACTTAATGGCTTGGGAGGAGGAGCT 1440  
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DB 1441 CTTTCCCATCTGCTGAATCATCTTCCCCACACACATCAATTCATATCTACTACCT 1500  
QY 1501 AACAGCAACACTGGGAGAGCCCTGAGCATTCGGACTTGGCCCTATGGGAGGAGGAGCT 1560  
DB 1501 AACAGCAACACTGGGAGAGCCCTGAGCATTCGGACTTGGCCCTATGGGAGGAGGAGCT 1560  
QY 1561 GGAGGAGTGGCTGCATGTATCTGATTAATACAGACCCCTGTC 1600  
DB 1561 GGAGGAGTGGCTGCATGTATCTGATTAATACAGACCCCTGTC 1600

## RESULT 2

AAF61560  
ID AAF61560 standard; DNA; 1600 BP.

XX

AC AAF61560;

XX

DT 29-JUN-2001 (first entry)

XX

DE Human PRV-1 encoding DNA.

XX

KW PRV-1; human; hemostatic; polycythemia rubra vera; antisense therapy;  
KW treatment; diagnosis; pancytopenia; bone-marrow; blood; growth factor;  
KW pancytopenia; hematopoietic system disorder; ds.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT 36..1349

FT /\*tag= a

FT /product= "PRV-1"

XX

PN DE19947010-A1.  
 XX  
 PD  
 XX 05-APR-2001.  
 XX  
 PF 30-SEP-1999; 99DB-01047010.  
 XX  
 PR 30-SEP-1999; 99DE-01047010.  
 XX  
 PA (UYFR-) UNIV FREIBURG.  
 XX  
 XX Pahl H;  
 PI  
 XX  
 XX WPI; 2001-246167/26.  
 DR P-PSDB; AAB70851.  
 XX  
 XX New cloned PRV-1 gene associated with polycythemia rubra vera, e.g.  
 PT useful for preparing antisense molecules or polypeptides for treatment or  
 PT diagnosis of disorders of the hematopoietic system.  
 XX  
 PS Claim 4; Fig 1; 10pp; German.  
 XX  
 CC This invention describes a novel cloned PRV-1 gene (I) which has  
 CC hemostatic activity and is associated with polycythemia rubra vera (PRV).  
 CC (I) is useful for: (1) producing a recombinant PRV-1 polypeptide; (2)  
 CC producing antisense molecules useful for diagnosis and treatment of PRV;  
 CC (3) preparing medicaments for treating pancytopenias and pancytopathies  
 CC of the bone-marrow and blood. The polypeptide is useful: (1) as a growth  
 CC factor for inducing hematopoietic stem cells to form erythroid colonies;  
 CC (2) for preparing medicaments for treating pancytopenias and  
 CC pancytopathies of the bone-marrow and blood; (3) for treating and/or  
 CC multiplying autologous cells and/or established cell lines ex vivo or in  
 CC vitro; and (4) for producing antibodies useful for diagnosis of PRV or  
 CC other disorders of the hematopoietic system. This sequence encodes the  
 CC human PRV-1 protein described in the invention  
 XX  
 SQ Sequence 1600 BP; 340 A; 490 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 100.0%; Score 1600; DB 4; Length 1600;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGCAGAAAGATTACAGCCACAGACGGGTCTATGAGCGGGTATTACTCTGGCCC 60  
 DB 1 AAAAGCAGAAAGATTACAGCCACAGACGGGTCTATGAGCGGGTATTACTCTGGCCC 60  
 QY 61 TCTTGGGGTTTCACTCCCACTGCCAGAGTGACGGGGTCTCTGCCAGTTTGGGACAG 120  
 DB 61 TCTTGGGGTTTCACTCCCACTGCCAGAGTGACGGGGTCTCTGCCAGTTTGGGACAG 120  
 QY 121 TTCAGCATGTGTGGAAGGTCTCCGACCTGCCCCGGAATGGACCCCTTAAGAACACCACT 180  
 DB 121 TTCAGCATGTGTGGAAGGTCTCCGACCTGCCCCGGAATGGACCCCTTAAGAACACCACT 180  
 QY 181 GCGACACGCGCTTTGGGGTGCAGGACACAGTTGATGTCTATTGAGAGCGGACCCCAAGTGA 240  
 DB 181 GCGACACGCGCTTTGGGGTGCAGGACACAGTTGATGTCTATTGAGAGCGGACCCCAAGTGA 240  
 QY 241 GCTTGTGTCTTCAAGGGTGTGACGGAGGCCAAGGACAGGACCCCGGCTCACTGAGC 300  
 DB 241 GCTTGTGTCTTCAAGGGTGTGACGGAGGCCAAGGACAGGACCCCGGCTCACTGAGC 300  
 QY 301 ACCGGATGGGCCCGGCTCTCCCTGATCTCCCTACACCTTCGTGTCGCGCAGGAGACT 360  
 DB 301 ACCGGATGGGCCCGGCTCTCCCTGATCTCCCTACACCTTCGTGTCGCGCAGGAGACT 360  
 QY 361 TCTGCAACCACTCGTTAACTCCCTCCGCTTTGGGCCCCACAGCCGCCACAGACCCAG 420  
 DB 361 TCTGCAACCACTCGTTAACTCCCTCCGCTTTGGGCCCCACAGCCGCCACAGACCCAG 420  
 QY 421 GATCTTTGAGTGCCCACTGTCTTGTCTATGAAAGGCTCTGTGGAGGGGACAAAGAAG 480  
 DB 421 GATCTTTGAGTGCCCACTGTCTTGTCTATGAAAGGCTCTGTGGAGGGGACAAAGAAG 480

QY 481 AGATCTGCCCAAGGGGACACACACTGTATTATGATGGCTCTCTCAGGCTCAGGGGAGGAG 540  
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 QY 541 GCATCTTCTCAATCTGAGAGTCCAGGGATGCAATGCCCCAGCCAGGTTGCAACCTGTCTCA 600  
 DB 541 GCATCTTCTCAATCTGAGAGTCCAGGGATGCAATGCCCCAGCCAGGTTGCAACCTGTCTCA 600  
 QY 601 ATGGGACACAGGAAATTTGGSCCGTGGTATGACTGAGAACTCAATAGGAAGATTTTC 660  
 DB 601 ATGGGACACAGGAAATTTGGSCCGTGGTATGACTGAGAACTCAATAGGAAGATTTTC 660  
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 DB 721 ATTGGACACATCGAATACCGAGATGTGGAGTGGGGGAGGTTGTCTCAGGACACGCTGC 780  
 QY 781 TGCTCATAGATGTAGGACTCACATCAACCTGTGGGGACAAAGGCTGCAGCACTCTTG 840  
 DB 781 TGCTCATAGATGTAGGACTCACATCAACCTGTGGGGACAAAGGCTGCAGCACTCTTG 840  
 QY 841 GGGCTCAAAATTTCCAGAAAGACCAACCATCCACTCAGCCCCCTCTGGGGTCTTTGTGSCCT 900  
 DB 841 GGGCTCAAAATTTCCAGAAAGACCAACCATCCACTCAGCCCCCTCTGGGGTCTTTGTGSCCT 900  
 QY 901 CTTATACCACTTCTCTCTCTCGGACCTGTGCAATAGTGCAGAGCAGGAGGTTCTGTC 960  
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 DB 961 TGAACCTCCCTCCCTCTCAAGCTGCCCTGTGCCAGGAGACCGGAGTGTCTTACCTGTG 1020  
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 DB 1021 TGAGGCCCCCTTGGAACTCTTCAAGTGGCTTCCCCCGGAATGACTCTGCCAGGGGCGCCA 1080  
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 DB 1141 TTTGAGGGCTCGCTGGGCCCAACCTTCCAGCTTCTTGTGTACACACAGACCAATCGGA 1200  
 QY 1201 TCTTCTCTCGCGGTGAGAAAGCGTGTGTCAGGCTCTCTGCTCTCAGCATGAGGAGGTG 1260  
 DB 1201 TCTTCTCTCGCGGTGAGAAAGCGTGTGTCAGGCTCTCTGCTCTCAGCATGAGGAGGTG 1260  
 QY 1261 GGGCTGAGGCGCTTGGAGTCTCTCACTTGGGGGGTGGGGTGGCACTGGCCCCCAGCGCTGT 1320  
 DB 1261 GGGCTGAGGCGCTTGGAGTCTCTCACTTGGGGGGTGGGGTGGCACTGGCCCCCAGCGCTGT 1320  
 QY 1321 GGTGGGAGTGGTTTGGCTTCTCTTAATTTACCCCGACGATTTCTTACCGCTGC 1380  
 DB 1321 GGTGGGAGTGGTTTGGCTTCTCTTAATTTACCCCGACGATTTCTTACCGCTGC 1380  
 QY 1381 TGACCAACCACTCAACCTCTGACTCAATAACCTTAATGGCTTTGACACCAAGATT 1440  
 DB 1381 TGACCAACCACTCAACCTCTGACTCAATAACCTTAATGGCTTTGACACCAAGATT 1440  
 QY 1441 CTTTCCCAATTTCTGTCATGAATCATTTTCCCAACACCAATCATTTCTACTACCT 1500  
 DB 1441 CTTTCCCAATTTCTGTCATGAATCATTTTCCCAACACCAATCATTTCTACTACCT 1500  
 QY 1501 AACAGCAACACTGGGGAGGCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGAGCT 1560  
 DB 1501 AACAGCAACACTGGGGAGGCTGGAGCATCCGGACTTGGCCCTATGGGAGAGGGAGCT 1560  
 QY 1561 GGAGGAGTGGCTGATGTATCTGATAATACAGACCCTGTC 1600

[illegible]

Db 1261 GGGCTGAGGCGCTGAGTCTCTCACTTGGGGGGTGGGCTGGCACTGGCCCCCGCGCTGT 1320  
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Db 1321 GGTGGGAGTGGTTTGGCCCTTCTGCTAACTATTAACCCCGAGATTCTTACCGCTGC 1380  
Qy 1381 TGACACCCACACTCAACCTCCCTCTGACCTCATAACTAATGGCCCTTGGACACAGATT 1440  
Db 1381 TGACACCCACACTCAACCTCCCTCTGACCTCATAACTAATGGCCCTTGGACACAGATT 1440  
Qy 1441 CTTTCCCATCTGTCGAATGATATCTTCCCAACACCAATCATATCTACTCACT 1500  
Db 1441 CTTTCCCATCTGTCGAATGATATCTTCCCAACACCAATCATATCTACTCACT 1500  
Qy 1501 AACAGCAACTGGGGAGCGCTGGAGCATCCGACTTGCCTATGGAGGGGAGCGT 1560  
Db 1501 AACAGCAACTGGGGAGCGCTGGAGCATCCGACTTGCCTATGGAGGGGAGCGT 1560  
Qy 1561 GGAGGAGTGGCTGATCTGATCTGATATACAGACCCCTGTC 1600  
Db 1561 GGAGGAGTGGCTGATCTGATCTGATATACAGACCCCTGTC 1600

## RESULT 4

AEA04409

ID AEA04409 standard; cDNA; 1630 BP.

AC AEA04409;

XX

XX

28-JUL-2005 (first entry)

XX

Human cDNA from gene under-expressed in cancer, PRV1.

XX

Tumor marker; ss; gene; colon tumor; cancer; cytostatic; neoplasm;

diagnostic; microarray; drug screening.

XX

Homo sapiens.

XX

WO2005044990-A2.

XX

19-MAY-2005.

XX

01-NOV-2004; 2004WO-US036404.

XX

04-NOV-2003; 2003US-00700439.

XX

(FARB ) BAYER HEALTHCARE LLC.

XX

(MAYO-) MAYO FOUND MEDICAL EDUCATION &amp; RES.

XX

Burgess C, Myerow S, Thiagalingam A, Maimonis P, Molino G;

XX

Burgart L, Boardman LA, Thibodeau S, Lewis M;

XX

WPI; 2005-372198/38.

XX

P-PSDB; AEA04502.

XX

REFSEQ; NM\_020406.

XX

Claim 1; SEQ ID NO 54; 256pp; English.

XX

The invention relates to detecting differential expression of one or more

nucleic acid sequences (appearing as AEA04356-AEA04448 in a biological

sample comprising obtaining the sample from a subject, and detecting a

change in the expression level of one or more nucleic acid sequences

relative to a control expression level of the nucleic acid sequences, is

new. Also included are detecting cancer (or a pre-malignant condition

thereof) in a subject (comprising comparing the expression level of one

or more nucleic acid sequences in a biological sample from the subject

with a control expression level of the nucleic acid sequences, where a

change of at least two-fold in the expression level of the nucleic acid

sequences is indicative of cancer or pre-malignant condition), monitoring the onset (or progression, or regression) of cancer (or a pre-malignant condition) in a subject (by detecting in a biological sample of the subject at a first point in time the expression of one or more nucleic acid sequences, repeating the first step at a subsequent point in time and comparing the expression level detected, where a change in the expression level is indicative of progression of cancer or its pre-malignant condition in the subject), determining prognosis for cancer or its pre-malignant condition in a subject (comprising detecting in a biological sample of the subject, the expression level of one or more nucleic acid sequences, comparing the expression level with a reference expression level of the nucleic acid sequences and evaluating the prognosis of the subject based on the comparison), determining the efficacy of a test compound for inhibiting cancer in a subject, determining the efficacy of a therapy for inhibiting cancer in a subject, selecting a composition for inhibiting cancer in a subject, inhibiting cancer in a subject, a polypeptide encoded by the nucleic acids above (appearing as AEA04449-AEA04541), an antibody that specifically binds to the polypeptide sequence, and detecting in a biological sample the presence of a polypeptide. The method is useful for detecting differential expression of one or more nucleic acid sequences in a biological sample, which is useful for detecting cancer (especially colon cancer), monitoring the onset, progression, or regression of cancer or a pre-malignant condition, or determining prognosis for cancer or its pre-malignant condition in a subject, or for determining the efficacy of a test compound for inhibiting cancer in a subject. The compound is useful for inhibiting cancer in a subject. The antibodies may also be used to treat cancer. The present sequence is a cDNA from a human gene under-expressed in cancer samples.

Sequence 1630 BP; 365 A; 492 C; 436 G; 336 T; 0 U; 1 Other;

Query Match 100.0%; Score 1600; DB 14; Length 1630;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAGCAGAAGAGATTACCAAGCCACAGACGGGTCTAGAGCGCGGTATTACTGTGGCCC 60  
Db 1 AAAAGCAGAAGAGATTACCAAGCCACAGACGGGTCTAGAGCGCGGTATTACTGTGGCCC 60  
Qy 61 TCCTGGGGTTTCATCTCCCACTGCCAGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120  
Db 61 TCCTGGGGTTTCATCTCCCACTGCCAGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAG 120  
Qy 121 TTGACGATGTGGAGGTGTCCGACCTGCCCGGCAATGGAACCCCTAAGAACACCACTGT 180  
Db 121 TTGACGATGTGGAGGTGTCCGACCTGCCCGGCAATGGAACCCCTAAGAACACCACTGT 180  
Qy 181 GCGACAGCGGCTTGGGGTGCAGGACACGTTGATGCTCATTGAGCGGACCCCAAGTGA 240  
Db 181 GCGACAGCGGCTTGGGGTGCAGGACACGTTGATGCTCATTGAGCGGACCCCAAGTGA 240  
Qy 241 GCCTGTGTCTCTCAAGGGCTGCACCGAGGCGCCCAAGGACCCAGGAGCCCGGTCTACTGAGC 300  
Db 241 GCCTGTGTCTCTCAAGGGCTGCACCGAGGCGCCCAAGGACCCAGGAGCCCGGTCTACTGAGC 300  
Qy 301 ACCGATGGGCGCGGCTCTCCCTGATCTCTTACACTTCTGTCGTCGCGCAGGAGACT 360  
Db 301 ACCGATGGGCGCGGCTCTCCCTGATCTCTTACACTTCTGTCGTCGCGCAGGAGACT 360  
Qy 361 TCTGCAACACCTCGTTAACTCCCTCCGCTTTGGGCCCCCACAGCCCGCCAGACCCAG 420  
Db 361 TCTGCAACACCTCGTTAACTCCCTCCGCTTTGGGCCCCCACAGCCCGCCAGACCCAG 420  
Qy 421 GATCTTTGAGTGGCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACACAGAG 480  
Db 421 GATCTTTGAGTGGCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAGGGGACACAGAG 480  
Qy 481 AGATCTGCCCAAGGGGACACACACTGTGATGCGCTCTCTCAGGCTCAGGGGAGAG 540  
Db 481 AGATCTGCCCAAGGGGACACACACTGTGATGCGCTCTCTCAGGCTCAGGGGAGAG 540  
Qy 541 GCATCTTCTCCATCTGAGAGTCAGGGATGTCATGCCCGCCAGGCTTGCAACTGTCTCA 600

Db 541 GCATCTTCTCAATCTGAGAGTCAGGGATGCGATGCCCGCAGCGGTGCAACCTGCTCA 600  
QY 601 ATGGGACACAGGAAATTTGGCCCGTGGGTATGATGAGAACTGCAATAGGAAGATTTTC 660  
Db 601 ATGGGACACAGGAAATTTGGCCCGTGGGTATGATGAGAACTGCAATAGGAAGATTTTC 660  
QY 661 TGACCTGTCTCATCGGGGACCAACATTATGACACACGMAAATTTGGCTCAAGAACCCACTG 720  
Db 661 TGACCTGTCTCATCGGGGACCAACATTATGACACACGMAAATTTGGCTCAAGAACCCACTG 720  
QY 721 ATTGGACCAATCCGAATACCGAGATGTGAGAGTGGGGCAGAGTGTGTCAAGGACACCTGC 780  
Db 721 ATTGGACCAATCCGAATACCGAGATGTGAGAGTGGGGCAGAGTGTGTCAAGGACACCTGC 780  
QY 781 TGCTCATAGATGTAGGACTCACATCAACCTGTGGGGACAAAAGCTGCAGCACTGTTG 840  
Db 781 TGCTCATAGATGTAGGACTCACATCAACCTGTGGGGACAAAAGCTGCAGCACTGTTG 840  
QY 841 GGGCTCAAAATTTCCAGAGACCAACCATCCACTCAGCCCTCTCTGGGGTCTTTGTGGCCT 900  
Db 841 GGGCTCAAAATTTCCAGAGACCAACCATCCACTCAGCCCTCTCTGGGGTCTTTGTGGCCT 900  
QY 901 CCTATACCCACTTCTGCTCGGACCTGTGCGACCTGTGCAATAGTGCACGACGAGCGTTCTGC 960  
Db 901 CCTATACCCACTTCTGCTCGGACCTGTGCGAATAGTGCACGACGAGCGTTCTGC 960  
QY 961 TGAACCTCCCTCCCTCCTCAGCTGCCCTGTGCCAGGAGCGGAGTGTCTTACCTGTG 1020  
Db 961 TGAACCTCCCTCCCTCCTCAGCTGCCCTGTGCCAGGAGCGGAGTGTCTTACCTGTG 1020  
QY 1021 TGCAGGCGCTTGGAACTGTCTCAAGTGGCTTCCCGCCGGAATGACCTGCCCCAGGGGGCCCA 1080  
Db 1021 TGCAGGCGCTTGGAACTGTCTCAAGTGGCTTCCCGCCGGAATGACCTGCCCCAGGGGGCCCA 1080  
QY 1081 CTCAATGTTATGATGGGTACATTCATCTCTCAGAGGTGGGTGTGCCACCAAAATGAGCA 1140  
Db 1081 CTCAATGTTATGATGGGTACATTCATCTCTCAGAGGTGGGTGTGCCACCAAAATGAGCA 1140  
QY 1141 TTCAGGGCTGCGTGGGCCCACTTCCAGCTTCTTGTGTACCAACACAGACAATCGGA 1200  
Db 1141 TTCAGGGCTGCGTGGGCCCACTTCCAGCTTCTTGTGTACCAACACAGACAATCGGA 1200  
QY 1201 TCTTCTCTGCGCTGGAAGCGTGATGTGAGCGCTCTCTGCTCTCAGCATGAGGGAGGTG 1260  
Db 1201 TCTTCTCTGCGCTGGAAGCGTGATGTGAGCGCTCTCTGCTCTCAGCATGAGGGAGGTG 1260  
QY 1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGT 1320  
Db 1261 GGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGT 1320  
QY 1321 GGTGGGAGTGGTGGCCCTCTCTGCTTAATCTTATCCCGCAGGATTTCTACCGCTGC 1380  
Db 1321 GGTGGGAGTGGTGGCCCTCTCTGCTTAATCTTATCCCGCAGGATTTCTACCGCTGC 1380  
QY 1381 TGACCAACCACTCAACCTCCCTCTGACCTCTAATGAGCGCTTGGACACCAAGATT 1440  
Db 1381 TGACCAACCACTCAACCTCCCTCTGACCTCTAATGAGCGCTTGGACACCAAGATT 1440  
QY 1441 CTTTCCCAATCTGTCCATGAATCATCTTCCCAACACAAATCATATCTACTACCT 1500  
Db 1441 CTTTCCCAATCTGTCCATGAATCATCTTCCCAACACAAATCATATCTACTACCT 1500  
QY 1501 AACGACCACTGGGGAGCGCTGGAGCATCCGAGCTTGGCCATATGGAGAGGGGAGCT 1560  
Db 1501 AACGACCACTGGGGAGCGCTGGAGCATCCGAGCTTGGCCATATGGAGAGGGGAGCT 1560  
QY 1561 GGAGGAGTGGCTGATGTATCTGATATACAGACCCCTGTC 1600  
Db 1561 GGAGGAGTGGCTGATGTATCTGATATACAGACCCCTGTC 1600

RESULT 5

ADQ24979  
ID ADQ24979 standard; DNA; 1692 BP.  
XX AC ADQ24979;  
XX DT 26-AUG-2004 (first entry)  
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 7799.  
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
XX db.  
XX Homo sapiens.  
XX PN WO2004048938-A2.  
XX PD 10-JUN-2004.  
XX PF 26-NOV-2003; 2003WO-US038193.  
XX PR 26-NOV-2002; 2002US-0429739P.  
XX PA (PROT-) PROTEIN DESIGN LABS INC.  
XX PI Aziz N, Ginsburg WM, Zlotnik A;  
XX WPI; 2004-441208/41.  
XX Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.  
XX Example 2; SEQ ID NO 7799; 210pp; English.  
XX The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytotstatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.  
XX SQ Sequence 1692 BP; 427 A; 493 C; 436 G; 336 T; 0 U; 0 Other;  
Query Match 99.9%; Score 1598.4; DB 12; Length 1692;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1599; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AAAAGCAGAAAGAGATTACAGCCACAGCGGTCTATGAGCGGGTATTACTGTGCCCC 60  
Db 1 AAAAGCAGAAAGAGATTACAGCCACAGCGGTCTATGAGCGGGTATTACTGTGCCCC 60  
QY 61 TCCTGGGGTTCATCTCCCACTGCCAGGAGTGAGGGGTGCTCTGCCAGTTTGGGACAG 120  
Db 61 TCCTGGGGTTCATCTCCCACTGCCAGGAGTGAGGGGTGCTCTGCCAGTTTGGGACAG 120  
QY 121 TTCAGCATGTGTGGAAGGTGTCCGACTGCCCGGCAATGGACCCCTTAAGAAACACCAAGCT 180  
Db 121 TTCAGCATGTGTGGAAGGTGTCCGACTGCCCGGCAATGGACCCCTTAAGAAACACCAAGCT 180  
QY 181 GCGACAGCGGCTTGGGGTGCAGGACACGTTGATGTCTTATTGAGAGCGGACCCCAAGTGA 240  
Db 181 GCGACAGCGGCTTGGGGTGCAGGACACGTTGATGTCTTATTGAGAGCGGACCCCAAGTGA 240  
QY 241 GCCTGTGTCTCTCAAGGGCTGCAGGAGCGGACAGGAGCCCGCGTCACTGAGC 300  
|||||

241 GCCTGTGCTCTCCAGGGCTGACGAGGCGCAAGGACACGAGGACCCCGGCTCACTGAGC 300  
Qy  
301 ACCGATGGGCGCGGCTCTCCCTGATCTCTACACCTTCTGTCGGCCAGGAGACT 360  
Db  
301 ACCGATGGGCGCGGCTCTCCCTGATCTCTACACCTTCTGTCGGCCAGGAGACT 360  
Qy  
361 TCTGCAACAACTCTGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGAGCCAG 420  
Db  
361 TCTGCAACAACTCTGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGAGCCAG 420  
Qy  
421 GATCTTGGAGTGGCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAAGGACAAACAAG 480  
Db  
421 GATCTTGGAGTGGCCAGTCTGCTTGTCTATGGAAGGCTGTCTGGAAGGACAAACAAG 480  
Qy  
481 AGATCTGCCCAAGGGACACACACTGTTATGATGCCCTCCTCAGGCTCAGGGGAGGAG 540  
Db  
481 AGATCTGCCCAAGGGACACACACTGTTATGATGCCCTCCTCAGGCTCAGGGGAGGAG 540  
Qy  
541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCAATGCCGCCAGCCAGGTTGCAACCTGCTCA 600  
Db  
541 GCATCTTCTCCAATCTGAGAGTCCAGGGATGCAATGCCGCCAGCCAGGTTGCAACCTGCTCA 600  
Qy  
601 ATGGGACACAGGAAATTTGGGCCCCGCTGGGTATGACTGAGAACTGCAATAGGAAGATTTTC 660  
Db  
601 ATGGGACACAGGAAATTTGGGCCCCGCTGGGTATGACTGAGAACTGCAATAGGAAGATTTTC 660  
Qy  
661 TGACCTGTCTCGGGGACCAACCAATATGACACAGGAATTTGGCTCAAGAACCCACTG 720  
Db  
661 TGACCTGTCTCGGGGACCAACCAATATGACACAGGAATTTGGCTCAAGAACCCACTG 720  
Qy  
721 ATTGGACACATCGAATACCGAGATGTCGAGGTGGGCGAGGTGTCTCAGGAGACGCTGC 780  
Db  
721 ATTGGACACATCGAATACCGAGATGTCGAGGTGGGCGAGGTGTCTCAGGAGACGCTGC 780  
Qy  
781 TGCTCATAGATAGGACTCACTCAACCTGTGTGGGACAAAGGCTGAGCACTGTTG 840  
Db  
781 TGCTCATAGATAGGACTCACTCAACCTGTGTGGGACAAAGGCTGAGCACTGTTG 840  
Qy  
841 GGGCTCAAAATTTCCAGAGACCAACCATCACTCAGCCCTCTCTGGGGTCTGTGGCT 900  
Db  
841 GGGCTCAAAATTTCCAGAGACCAACCATCACTCAGCCCTCTCTGGGGTCTGTGGCT 900  
Qy  
901 CCTATACCACTTCTGTCTCTCGGACCTGTGCAATAGTGGCAGCAGCAGCGTTCCTGC 960  
Db  
901 CCTATACCACTTCTGTCTCTCGGACCTGTGCAATAGTGGCAGCAGCAGCGTTCCTGC 960  
Qy  
961 TGAACCTCCCTCCCTCTCAAGTGGCCCTGTCCAGGAGACCGGACGTCTTACCTGTG 1020  
Db  
961 TGAACCTCCCTCCCTCTCAAGTGGCCCTGTCCAGGAGACCGGACGTCTTACCTGTG 1020  
Qy  
1021 TGCAGCCCTTGGAACTGTTCAAGTGGCTCCCGCCGAATGACCTGCCCGAGGGGCGCA 1080  
Db  
1021 TGCAGCCCTTGGAACTGTTCAAGTGGCTCCCGCCGAATGACCTGCCCGAGGGGCGCA 1080  
Qy  
1081 CTCACTGTATGATGGGTACATTCATCTCTCAGGAGTGGCTGTCCACCAAAATGAGCA 1140  
Db  
1081 CTCACTGTATGATGGGTACATTCATCTCTCAGGAGTGGCTGTCCACCAAAATGAGCA 1140  
Qy  
1141 TTCAAGGCTCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCAACAGACAAATCGGGA 1200  
Db  
1141 TTCAAGGCTCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCAACAGACAAATCGGGA 1200  
Qy  
1201 TCTTCTCTGGCGTGAAGCGGTATGTGAGCCTCTCTGCTCTCAGCATGAGGAGGTG 1260  
Db  
1201 TCTTCTCTGGCGTGAAGCGGTATGTGAGCCTCTCTGCTCTCAGCATGAGGAGGTG 1260  
Qy  
1261 GGGCTGAGGCGCTGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCGAGCGCTGT 1320  
Db  
1261 GGGCTGAGGCGCTGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCGAGCGCTGT 1320  
Qy  
1321 GGTGGGAGTGGTTTGGCTTCTCTGCTTAACCTATTACCCCGAGATTTCTACCGCTGC 1380  
Db  
1321 GGTGGGAGTGGTTTGGCTTCTCTGCTTAACCTATTACCCCGAGATTTCTACCGCTGC 1380

1381 TGACCCACACACTCAACCTCCCTCTGACCTCTAATGCTTAACCTAATGSCCTTGGACACAGATT 1440  
Db  
1381 TGACCCACACACTCAACCTCCCTCTGACCTCTAATGCTTAACCTAATGSCCTTGGACACAGATT 1440  
Qy  
1441 CTTTCCCATCTCTGTCCATGAATCATCTTCCCAACACACAAATCATCTATCTACTCAGCT 1500  
Db  
1441 CTTTCCCATCTCTGTCCATGAATCATCTTCCCAACACACAAATCATCTATCTACTCAGCT 1500  
Qy  
1501 AACAGCAACACTGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGAGAGGGAGCGCT 1560  
Db  
1501 AACAGCAACACTGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGAGAGGGAGCGCT 1560  
Qy  
1561 GAGGAGTGGCTGCTATCTATCTGATAATACAGACCTCTGTC 1600  
Db  
1561 GAGGAGTGGCTGCTATCTGATAATACAGACCTCTGTC 1600

RESULT 6  
ABA97156  
ID ABA97156 standard; cDNA to mRNA; 1612 BP.  
XX  
AC ABA97156;  
XX  
DT 17-APR-2002 (first entry)  
XX  
XX Human granulocyte HNA-2a antigen cDNA.  
DE  
XX Human; gene; neutrophilic granulocyte; chromosome 19; HNA-2a; antigen;  
KW human neutrophil antigen-2a; NB-1 antigenic determination; diagnosis;  
KW alloantibody detection; neonatal; immunoneutropenia; iatrogenic;  
KW transplant-associated acute pulmonary insufficiency;  
KW bone marrow transplant; autoimmune neutropenia; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH CDS 28..1341  
FT /\*tag= C  
FT /product= "HNA-2a antigen (previously called NB-1)"  
FT sig\_peptide 28..90  
FT /\*tag= a  
FT mat\_peptide 91..1338  
FT /\*tag= b  
XX  
PN DE1028725-A1.  
XX  
PD 13-DEC-2001.  
XX  
PF 09-JUN-2000; 2000DE-01028725.  
XX  
PR 09-JUN-2000; 2000DE-01028725.  
XX  
PA (BUXJ/) BUX J.  
XX  
PI Bux J, Kissel K;  
XX  
DR WPI; 2002-148930/20.  
XX  
DR P-PSDB; AAG80767.  
XX  
PT Primary structure and nucleic acid of the human neutrophil antigen-2a,  
PT useful for antigen detection, e.g. diagnosis of various forms of  
PT neutropenia.  
XX  
PS Disclosure; Page 4-6; 8pp; German.  
XX  
CC This invention describes the human neutrophil antigen-2a (HNA-2a,  
CC previously described as NB-1), expressed on neutrophilic granulocytes.  
CC The nucleic acid and amino acid sequences of HNA-2a are used in RNA- or  
CC DNA-based methods of antigen determination, e.g. polymerase chain  
CC reaction with sequence-specific primers, hybridisation with sequence-  
CC specific oligonucleotides or DNA sequencing. They are also used for  
CC recombinant production of the antigen for detection of specific



CC	alloantibodies. Allo- and auto-antibodies against HNA-2a are implicated
CC	in neonatal immunoneutropenia, transplant-associated acute pulmonary
CC	insufficiency, immunoneutropenia after bone marrow transplant,
CC	iatrogenic immunoneutropenia and autoimmunoneutropenia. Using HNA-2a,
CC	or its nucleic acid, for diagnosis, overcomes the stability problems
CC	associated with use and transport of very unstable granulocytes. The
CC	nucleic acid also allows large-scale production of the antigen. This
CC	sequence encodes the human granulocyte HNA-2a (NB-1) antigen found on
CC	chromosome 19 described in the invention
XX	
SQ	Sequence 1612 BP; 351 A; 491 C; 433 G; 337 T; 0 U; 0 Other;
	Query Match 99.0%; Score 1584; DB 6; Length 1612;
	Best Local Similarity 99.7%; Pred. No. 0;
	Matches 1587; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy	9 AAAGAGATTACACGCCACAGACGGGTGATGACCGCGGTATTACTGCTGGCCCTCTCGGG 68
Db	1 AAAGAGATTACACGCCACAGACGGGTGATGACCGCGGTATTACTGCTGGCCCTCTCGGG 60
Qy	69 TTGATCTCCACTGCCAGGAGTGCAGGCGTGCTCTGCCAGTTTGGACAGTTTCAGCAT 128
Db	61 TTGATCTCCACTGCCAGGAGTGCAGGCGTGCTCTGCCAGTTTGGACAGTTTCAGCAT 120
Qy	129 GTGTGGAAGGTGTCGACCTGCCCGGCAATGGAACCCCTAAGAAACACCAAGCTGCGACAGC 188
Db	121 GTGTGGAAGGTGTCGACCTGCCCGGCAATGGAACCCCTAAGAAACACCAAGCTGCGACAGC 180
Qy	189 GGCCTTGGGTGCCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCGCTGGTG 248
Db	181 GGCCTTGGGTGCCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCGCTGGTG 240
Qy	249 CTCTCCRAAGGCTCAGCGAGGCCAAGAACACAGAGCCCCCGCTCACTGAGCACCGGATG 308
Db	241 CTCTCCRAAGGCTCAGCGAGGCCAAGAACACAGAGCCCCCGCTCACTGAGCACCGGATG 300
Qy	309 GGCCCCGGCCCTCTCCCTGATCTCCTTACA CTTTGTGTGTCGCCCCAGGAGGACTTCTGCAAC 368
Db	301 GGCCCCGGCCCTCTCCCTGATCTCCTTACA CTTTGTGTGTCGCCCCAGGAGGACTTCTGCAAC 360
Qy	369 AACCTGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGACACCCAGGATCTCTTG 428
Db	361 AACCTGTTAACTCCCTCCCGCTTTGGGCCCCCAGACCCCCCAGAGATCTCTTG 420
Qy	429 AGGTGCCCAGCTGCTGTTCTATGGAAGGCTGTCTGGAGGGGACAAACAGAGAGATCTGC 488
Db	421 AGGTGCCCAGCTGCTGTTCTATGGAAGGCTGTCTGGAGGGGACAAACAGAGAGATCTGC 480
Qy	489 CCCAAGGGGACACACACTGTTTATGATGGCTCTCTCAGGCTCAGGGAGGAGGATCTTC 548
Db	481 CCCAAGGGGACACACACTGTTTATGATGGCTCTCTCAGGCTCAGGGAGGAGGATCTTC 540
Qy	549 TCCAATCTGAGAGTCCAGGGATGATGCCCCCAGCCAGGTTCGCAACCTGCTCAATGGGACA 608
Db	541 TCCAATCTGAGAGTCCAGGGATGATGCCCCCAGCCAGAGTTGCAACCTGCTCAATGGGACA 600
Qy	609 CAGGAAATTTGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAGAATTTTCTGACCTGT 668
Db	601 CAGGAAATTTGGCCCGTGGGTATGACTGAGAACTGCAATAGGAAGAATTTTCTGACCTGT 660
Qy	669 CATCGGGGACACCATTTATGACACCGGAACTTTGGCTCAAGAACCCACTGATTTGGACC 728
Db	661 CATCGGGGACACCATTTATGACACCGGAACTTTGGCTCAAGAACCCACTGATTTGGACC 720
Qy	729 ACATCGAATACCGAGATGTGCGAGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCAT 788
Db	721 ACATCGAATACCGAGATGTGCGAGTGGGGCAGGTGTGTCAGGAGACGCTGCTGCTCAT 780
Qy	789 GATGTAGACTCAGATCAACCCCTGTTGGGACAAAGAAGCTCGACACTGTTGGGCTCAA 848
Db	781 GATGTAGACTCAGATCAACCCCTGTTGGGACAAAGAAGCTCGACACTGTTGGGCTCAA 840
Qy	849 AATTCCAGAGAGACCAACCATCACTCAGCCCCCTCTCTGGGGTGCTTTGTGGCTCTCTATACC 908





XX PS Claim 2; Fig 249; 822pp; English.

XX CC The invention provides membrane-bound PRO polypeptides and

CC polynucleotides encoding them. The PRO sequences of the invention were

CC identified based on extracellular domain homology screening. The PRO

CC sequences have homology with proteins including LDL receptors, TIE

CC ligands and various enzymes. The membrane-bound proteins and receptor

CC molecules are useful as pharmaceutical and diagnostic agents. Receptor

CC immunoadhesins, for instance, can be used as therapeutic agents to block

CC receptor-ligand interactions. The membrane-bound proteins can also be

CC employed for screening of potential peptide or small molecule inhibitors

CC of the relevant receptor/ligand interaction. The PRO encoding sequences

CC are useful as hybridization probes, in chromosome and gene mapping and in

CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will

CC also be useful for the preparation of PRO polypeptides, especially by

CC recombinant techniques

XX SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 3; Length 1587;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGCCACAGACGGGTATGAGCGCGGTATTTACTGCTGGCCCTCCTGGGGTTCACTCC 79

DB 1 CAGCCACAGACGGGTATGAGCGCGGTATTTACTGCTGGCCCTCCTGGGGTTCACTCC 60

QY 80 ACTGCCAGGAGTCAGCGCGTCTCTGCCAGTTTGGGACAGTTGAGCATGTGGAGGT 139

DB 61 ACTGCCAGGAGTCAGCGCGTCTCTGCCAGTTTGGGACAGTTGAGCATGTGGAGGT 120

QY 140 GTCCGACCTGCCCGGCAATGAGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTG 199

DB 121 GTCCGACCTACCCCGGCAATGAGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTG 180

QY 200 CCAGGACAGCTTGATGCTCATGAGCGCGACCCCAAGTGAGCCTGGTCTCTCCAAAGG 259

DB 181 CCAGGACAGCTTGATGCTCATGAGCGCGACCCCAAGTGAGCCTGGTCTCTCCAAAGG 240

QY 260 CTGACGGAGGCCAAGGACCCAGGACCCCGCTCACTGACGACGGATGGGCGCCGCGCT 319

DB 241 CTGACGGAGGCCAAGGACCCAGGACCCCGCTCACTGACGACGGATGGGCGCCGCGCT 300

QY 320 CTCCCTGATCTCTACACCTTCTGCTGCCGCCAGGAGGACTTCTGCAACCAACCTCGTTAA 379

DB 301 CTCCCTGATCTCTACACCTTCTGCTGCCGCCAGGAGGACTTCTGCAACCAACCTCGTTAA 360

QY 380 CTCCCTCCCGCTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCCTTGAGGTGCCAGT 439

DB 361 CTCCCTCCCGCTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCCTTGAGGTGCCAGT 420

QY 440 CTGCTGCTATGAGAGGCTCTGAGAGGGGACACAGAGAGATCTGCCCCCAAGGGGAC 499

DB 421 CTGCTGCTATGAGAGGCTCTGAGAGGGGACACAGAGAGATCTGCCCCCAAGGGGAC 480

QY 500 CACACACTGTTATGAGGCTCTCAGGCTCAGGGAGGAGGACTTCTTCCCAATCTGAG 559

DB 481 CACACACTGTTATGAGGCTCTCAGGCTCAGGGAGGAGGACTTCTTCCCAATCTGAG 540

QY 560 AGTCCAGGAGTATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGAAATTTGG 619

DB 541 AGTCCAGGAGTATGCCCCAGCCAGGTTGCAACCTGCTCAATGGGACACAGAAATTTGG 600

QY 620 GCCCGTGGGTATGACTGAGAACTTGGCTCAAGAACCCACCTGATTTGGACCATCGAATAC 739

DB 601 GCCCGTGGGTATGACTGAGAACTTGGCTCAAGAACCCACCTGATTTGGACCATCGAATAC 720

QY 680 CACCATTTATGACACACGGAACCTTGGCTCAAGAACCCACCTGATTTGGACCATCGAATAC 739

DB 661 CACCATTTATGACACACGGAACCTTGGCTCAAGAACCCACCTGATTTGGACCATCGAATAC 720

QY 740 CGAGATGTGCGAGGTGGGCGAGGTGTGTCAGGAGACGCTGCTCATAGATGTAGGACT 799

DB 721 CGAGATGTGCGAGGTGGGCGAGGTGTGTGAGGAGACGCTGCTCATATAGTAGGACT 780

QY 800 CACATCAACCCCTGCTGGGACAAAAGGCTGACAGACTGTTGGGCTCAAAATTTCCAGAA 859

DB 781 CACATCAACCCCTGCTGGGACAAAAGGCTGACAGACTGTTGGGCTCAAAATTTCCAGAA 840

QY 860 GACCACCATCCACTCAGCCCCCTCCTGGGGTGTCTTGGGCTCCTATACCCACTTCTGCTC 919

DB 841 GACCACCATCCACTCAGCCCCCTCCTGGGGTGTCTTGGGCTCCTATACCCACTTCTGCTC 900

QY 920 CTGCGACCTGTGCAATAGTGCACAGCAGCAGCGTTCTGCTGAACCTCCCTCCTCTCA 979

DB 901 CTGCGACCTGTGCAATAGTGCACAGCAGCAGCGTTCTGCTGAACCTCCCTCCTCTCA 960

QY 980 AGCTGCCCTGTGCCAGGAGACCGGCGAGTGTCTTACTGCTGTCAGGCCCCCTTGGAACTG 1039

DB 961 AGCTGCCCTGTGCCAGGAGACCGGCGAGTGTCTTACTGCTGTCAGGCCCCCTTGGAACTG 1020

QY 1040 TTCAAGTGTCTCCCCCGAATGACCTGCCCGGCGGCGGCGGCTCATTTGTTATGATGGTA 1099

DB 1021 TTCAAGTGTCTCCCCCGAATGACCTGCCCGGCGGCGGCGGCTCATTTGTTATGATGGTA 1080

QY 1100 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159

DB 1081 CATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140

QY 1160 ACCTTCCAGCTTCTTGTGAACCCACACACAGACAAATCGGGATCTTCTCGCGGTGAGAA 1219

DB 1141 ACCTTCCAGCTTCTTGTGAACCCACACACAGACAAATCGGGATCTTCTCGCGGTGAGAA 1200

QY 1220 GCGTGTGTCAGCCTCTGCTCCTCAGCATGAGGAGGTGGGGCTGAGGGCTTGGAGTC 1279

DB 1201 GCGTGTGTCAGCCTCTGCTCCTCAGCATGAGGAGGTGGGGCTGAGGGCTTGGAGTC 1260

QY 1280 TCTCAGTGGGGGTGGGGCTGGGCTGCGCTGCGGCTGCTGCTGAGGAGTGGTGGGCTTGGCC 1339

DB 1261 TCTCAGTGGGGGTGGGGCTGGGCTGCGCTGCGGCTGCTGCTGAGGAGTGGTGGGCTTGGCC 1320

QY 1340 TTCTGCTAACTTATTAGCCCCCAGCATTTCTTCCCGCTGCTGACCAACCCACTCAACC 1399

DB 1321 TTCTGCTAACTTATTAGCCCCCAGCATTTCTTCCCGCTGCTGACCAACCCACTCAACC 1380

QY 1400 TCCCTCTGACCTCATAACTTAATGGCTTGGACACAGAGTTCTTCCATCTGTCATG 1459

DB 1381 TCCCTCTGACCTCATAACTTAATGGCTTGGACACAGAGTTCTTCCATCTGTCATG 1440

QY 1460 AATCATCTTCCCGACACACAAATCATATCTACTCACTCACTCACTCACTCACTCACTCA 1519

DB 1441 AATCATCTTCCCGACACACAAATCATATCTACTCACTCACTCACTCACTCACTCACTCA 1500

QY 1520 GCTGAGCATCGGACTTGGCTTATGGAGAGGGGACGCTGAGGAGTGGCTGCTGATGTA 1579

DB 1501 GCTGAGCATCGGACTTGGCTTATGGAGAGGGGACGCTGAGGAGTGGCTGCTGATGTA 1560

QY 1580 TCTGATAATACAGACCTTGTGTC 1600

DB 1561 TCTGATAATACAGACCTTGTGTC 1581

RESULT 8

AAA51263

ID AAA51263 standard; cDNA; 1587 BP.

XX

AC AAA51263;

XX

DT 26-SEP-2000 (first entry)

XX

DE Human DNA encoding PRO1863, a novel transmembrane protein.

XX

KW PRO1863; secreted protein; transmembrane protein; recombinant production;

XX

gene therapy; ss.

XX

OS Homo sapiens.  
XX Key Location/Qualifiers  
FH 17..1330  
FT /\*tag=a  
FT /product= "PRO1863"  
FT /note= "A novel transmembrane protein"  
FT 17..61  
FT sig\_peptide /\*tag= b  
XX  
XX W0200036102-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 01-DEC-1999; 99WO-US028634.  
XX  
XX 16-DEC-1998; 98US-0112851P.  
XX 16-DEC-1998; 98US-0113145P.  
XX 22-DEC-1998; 98US-0113511P.  
XX 12-JAN-1999; 99US-0115558P.  
XX 12-JAN-1999; 99US-0115565P.  
XX 12-JAN-1999; 99US-0115733P.  
XX 09-FEB-1999; 99US-0119341P.  
XX 10-FEB-1999; 99US-0119537P.  
XX 12-FEB-1999; 99US-0119665P.  
XX 02-JUN-1999; 99WO-US012252.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;  
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2000-431586/37.  
DR P-PSDB; AAY96733.  
XX  
XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a  
transmembrane polypeptide.  
XX  
XX Claim 1; Fig 9; 154pp; English.  
XX  
XX This cDNA encodes PRO1863, a novel transmembrane protein. The invention  
concerns novel secreted and transmembrane proteins, designated PRO  
polypeptides. The cDNA and gene sequences are useful in the recombinant  
production of PRO polypeptides, as a hybridization probe to screen  
libraries to isolate cDNAs with sequence identity to PRO polypeptides or  
CC to map the gene encoding the PRO polypeptides and analyzing genetic  
disorders. The cDNA/gene can also be used to produce transgenic animals  
CC useful for the development and screening of therapeutically useful  
CC reagents. They can also be used in gene therapy, e.g. to replace a  
defective gene  
XX  
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;  
Query Match 98.7%; Score 1579.4; DB 3; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX 20 CAGCCACAGACGGGTCTATGAGCGGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCCC 79  
DB 1 CAGCCACAGACGGGTCTATGAGCGGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCCC 60  
XX 80 ACTGCCAGGAGTGCAGCGGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAAGGT 139  
DB 61 ACTGCCAGGAGTGCAGCGGTCTCTGCCAGTTTGGACAGTTTCAGCATGTGTGGAAGGT 120  
XX 140 GTCGACCTCCCGGCAATGGACCCCTAAGAACACAGCTGCGACAGCGCTTTGGGGTG 199  
DB 121 GTCGACCTACCCGGCAATGGACCCCTAAGAACACAGCTGCGACAGCGCTTTGGGGTG 180  
XX 200 CCAGGACACGTTGATGTCTATTGAGAGCGGACCCCAAGTAGGCTGTGTCTTCCAGGG 259  
DB 181 CCAGGACACGTTGATGTCTATTGAGAGCGGACCCCAAGTAGGCTGTGTCTTCCAGGG 240

QY 260 CTGCACGGAGGCAAGGACAGGAGCCCGCTCACTGAGCACCGGATGGCCCCCGGCT 319  
DB 241 CTGCACGGAGGCAAGGACAGGAGCCCGCTCACTGAGCACCGGATGGCCCCCGGCT 300  
QY 320 CTCCTGATCTCTTACACCTTGTGTCGCGCAGGAGGACTTCTGCAACAACTCTGTAA 379  
DB 301 CTCCTGATCTCTTACACCTTGTGTCGCGCAGGAGGACTTCTGCAACAACTCTGTAA 360  
QY 380 CTCCTCCCGCTTGGGCCCCCAGAGCCCCCAGAGAGCCAGGATCTTGAAGTCCCACT 439  
DB 361 CTCCTCCCGCTTGGGCCCCCAGAGCCCCCAGAGAGCCAGGATCTTGAAGTCCCACT 420  
QY 440 CTGCTTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGAGAGATCTGCCCCCAAGGGAC 499  
DB 421 CTGCTTCTATGGAAGGCTGTCTGGAGGGGCAACAGAGAGAGATCTGCCCCCAAGGGAC 480  
QY 500 CACACCTGTTATGATGAGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCAATCTGAG 559  
DB 481 CACACCTGTTATGATGAGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCAATCTGAG 540  
QY 560 AGTCCAGGAGTGCATGCCCGCAGCAGGTTGCACTGCTCAATGGGACACAGGAAATGG 619  
DB 541 AGTCCAGGAGTGCATGCCCGCAGCAGGTTGCACTGCTCAATGGGACACAGGAAATGG 600  
QY 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGAC 679  
DB 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGAC 660  
QY 680 CACCATTTATGACACACGAGAACTTGGCTCAAGAACCCCACTGATTGGACCAATCGAATAC 739  
DB 661 CACCATTTATGACACACGAGAACTTGGCTCAAGAACCCCACTGATTGGACCAATCGAATAC 720  
QY 740 CGAGATGTCGAGGTGGGGCAGGTGTCTCAGGAGACGCTGCTCTATAGATGAGACT 799  
DB 721 CGAGATGTCGAGGTGGGGCAGGTGTCTCAGGAGACGCTGCTCTATAGATGAGACT 780  
QY 800 CACATCAACCTTGTGGGGCAAAAGGCTGCAGCAGCTTTGGGGCTCAAAATTCAGAA 859  
DB 781 CACATCAACCTTGTGGGGCAAAAGGCTGCAGCAGCTTTGGGGCTCAAAATTCAGAA 840  
QY 860 GACCACCATCACTCAGCCCCCTCTCTGGGGTGTCTTGGGGCTCTCTATACCACTTCTGCTC 919  
DB 841 GACCACCATCACTCAGCCCCCTCTCTGGGGTGTCTTGGGGCTCTCTATACCACTTCTGCTC 900  
QY 920 CTGGAGCTGTGCAATAGTCCAGCAGCAGAGGCTTCTGCTGAATCTCCCTCCCTCTCA 979  
DB 901 CTGGAGCTGTGCAATAGTCCAGCAGCAGAGGCTTCTGCTGAATCTCCCTCCCTCTCA 960  
QY 980 AGCTGCCCTGTCTCCAGGAGACCGGAGTCTCTTACCTGTGTCAGCCCCCTTGGAACTG 1039  
DB 961 AGCTGCCCTGTCTCCAGGAGACCGGAGTCTCTTACCTGTGTCAGCCCCCTTGGAACTG 1020  
QY 1040 TTCAAGTGGCTCCCCCGAATGACCTGCCCGAGGGGCGCACTCATTTGTTATGATGGTA 1099  
DB 1021 TTCAAGTGGCTCCCCCGAATGACCTGCCCGAGGGGCGCACTCATTTGTTATGATGGTA 1080  
QY 1100 CATTCATCTCTCAGGAGGTGGGTGTCCACAAATGAGCATTCAGGGCTGCGTGGCCCA 1159  
DB 1081 CATTCATCTCTCAGGAGGTGGGTGTCCACAAATGAGCATTCAGGGCTGCGTGGCCCA 1140  
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DB 1141 ACCTTCAGCTTCTTGTGAACACACAGCAAAATCGGATCTTCTCTGCGCGTGAA 1200  
QY 1220 GCGTGTATGTGAGCTCTCTCAGCATGAGGAGGTGGGGCTCAGGGCTCAGGAGTGC 1279  
DB 1201 GCGTGTATGTGAGCTCTCTGCTCTCAGCATGAGGAGGTGGGGCTCAGGAGTGC 1260  
QY 1280 TCTCATTGGGGGTGGGGCTGGCACTGGCCCCCAGCGCTGTGTGGGGAGTGGTTGCC 1339  
DB 1261 TCTCATTGGGGGTGGGGCTGGCACTGGCCCCCAGCGCTGTGTGGGGAGTGGTTGCC 1320

Qy	1340	TTCTGTCTAACTCTATTACCCACAGATCTTTACCGCTGCTGACACCCACACTCAACC	1399
Db	1321	TTCTGTCTAACTCTATTACCCACAGATCTTTACCGCTGCTGACACCCACACTCAACC	1380
Qy	1400	TCCCTCTGACTCTATAACCTTAATGGCCCTTGGACACACAGATTCTTTTCCCATTTCTGTCCATG	1459
Db	1381	TCCCTCTGACTCTATAACCTTAATGGCCCTTGGACACACAGATTCTTTTCCCATTTCTGTCCATG	1440
Qy	1460	AATCATCTTTCGCCACACACAAATCATTTATATCTACTCACTTAACAGGAAACACTGGGGAGA	1519
Db	1441	AATCATCTTTCGCCACACACAAATCATTTATATCTACTCACTTAACAGGAAACACTGGGGAGA	1500
Qy	1520	GCCTGGAGCATCCGAGCTTGCCTTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1579
Db	1501	GCCTGGAGCATCCGAGCTTGCCTTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1560
Qy	1580	TCTGATAATACAGACCCCTGTC	1600
Db	1561	TCTGATAATACAGACCCCTGTC	1581

RESULT 9  
AAS21476  
ID AAS21476 standard; cDNA; 1587 BP.

24-OCT-2001 (first entry)

DE Human cDNA sequence encoding for PRO1181 polypeptide.

Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 A-peptide; factor VIIA; gene therapy; ss.

XX Homo sapiens.

XX PN WO200140466-A2.

07-JUN-2001.

XX 01-DEC-2000: 2000WO-US032678.

XX  
PR 01-DEC-1999: 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634;  
PR 02-DEC-1999; 99WO-US028551;

PR 02-DEC-1999; 99WO-US028564;  
PR 02-DEC-1999; 99WO-US028565;

PR 09-DEC-1999; 99US-017026ZF.  
PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911:  
PR 20-DEC-1999; 99WO-US030999:

PR 30-DEC-1999; 99WO-US031243:  
PR 30-DEC-1999; 99WO-US031274:

PK 03-JAN-2000; 2000WC-US000213:  
PR 06-JAN-2000; 2000WC-US000277:

PR 06-JAN-2000; 2000WO-US000378;  
PR 11-FEB-2000; 2000WO-US003565;

PR 18-FEB-2000; 2000WO-US0004341.  
PR 18-FEB-2000; 2000WO-US0004342.

PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.

PK Z4-FEB-2000; 2000WO-US003004;  
PR 01-MAR-2000; 2000WO-US005601;

PR 03-MAR-2000; 2000US-0187202P.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 03-MAR-2000; 2000US-0187202P.

FR 10-MAR-2000; 2000WO-US0006315.  
PR 15-MAR-2000; 2000WO-US0006884.

20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.

Query Match	98.7%	Score 1579.4	DB 4	Length 1587
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1580; Conservative	0	Mismatches	1	Indels 0; Gaps 0

QY 20 CAGCCACAGACGGGTCTATGAGCGCGGTATTATCTGCTGGCCCTCTCTGGGGTTCATCTCTCC 79

Dp 1 CAGCCACAGACGGGTCTATGAGCGCGGTATTATCTGCTGGCCCTCTCTGGGGTTCATCTCTCC 60

QY 80 ACTGCCAGGATGCAGGCGTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGGAAGGT 139

ph 61 ACTGCCAGGATGCAGGCGTCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGGAAGGT 120

QY 140 GTCGCACTGCCCGGAATGACCCCTAAGAACACCAAGCTGCACAGCGGCTTGGGGTG 199

ph 121 GTCGCACTACCCCGGAATGACCCCTAAGAACACCAAGCTGCACAGCGGCTTGGGGTG 180

Qy	200	CCAGGACA	CGTTGATGCT	CATTGAGAGCGG	CCCCAAGTGAGCCT	GGTGCTCTCC	AAGGG	259
ph	181	CCAGGACA <td>CGTTGATGCT <td>CATTGAGAGCGG <td>CCCCAAGTGAGCCT <td>GGTGCTCTCC <td>AAGGG <td>240</td> </td></td></td></td></td>	CGTTGATGCT <td>CATTGAGAGCGG <td>CCCCAAGTGAGCCT <td>GGTGCTCTCC <td>AAGGG <td>240</td> </td></td></td></td>	CATTGAGAGCGG <td>CCCCAAGTGAGCCT <td>GGTGCTCTCC <td>AAGGG <td>240</td> </td></td></td>	CCCCAAGTGAGCCT <td>GGTGCTCTCC <td>AAGGG <td>240</td> </td></td>	GGTGCTCTCC <td>AAGGG <td>240</td> </td>	AAGGG <td>240</td>	240

Qy	260	CTGCA CGAGGCCAAGGACAGAGGCCCGCGTCACTGAGCACCGGATGGGCCCGGGCT	319
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320 CTCCTGATCTCCTACACCTTCTGTTGCCCGCAGGAGCACTTCTGCAACAACTCGTTAA 379
301 CTCCTGATCTCCTACACCTTCTGTTGCCCGCAGGAGCACTTCTGCAACAACTCGTTAA 360
380 CTCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGTAGGTGCCCCAGT 439
361 CTCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTGTAGGTGCCCCAGT 420
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1220 GCGTGTATGTCAGCTTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTCGGATC 1279
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1340 TTCTGTCTAATCTTATTAACCCACAGGATCTTCAACCGCTGCTGACCAACCACTCAACC 1399
1321 TTCTGTCTAATCTTATTAACCCACAGGATCTTCAACCGCTGCTGACCAACCACTCAACC 1380

1400 TCCTCTGAGCTCATTAACCTTAATGGCTTGGACACAGATTTCTTCCATTCTGTCCATG 1459
1381 TCCTCTGAGCTCATTAACCTTAATGGCTTGGACACAGATTTCTTCCATTCTGTCCATG 1440
1460 AATCATCTTCCCACACACAAATCATTTCAATCTACTCACCCTAACAGCAACACTGGGAGA 1519
1441 AATCATCTTCCCACACACAAATCATTTCAATCTACTCACCCTAACAGCAACACTGGGAGA 1500
1520 GCCTGGAGCATCCGGAATCTGCTTGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579
1501 GCCTGGAGCATCCGGAATCTGCTTGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560
1580 TCTGATAATACAGACCTGTGTC 1600
1561 TCTGATAATACAGACCTGTGTC 1581

RESULT 10
AAF44229
ID AAF44229 standard; cdna; 1587 BP.
XX
AAF44229;
AC
XX
02-APR-2001 (first entry)
DT
XX
Human PRO1181 (UNQ595) nucleotide sequence SEQ ID NO:354.
DE
XX
Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW
cancer; chromosomal mapping; gene mapping; tissue typing;
KW
diagnostic assay; ss.
XX
Homo sapiens.
XX
WO200073454-A1.
XX
07-DEC-2000.
XX
30-MAR-2000; 2000WO-US008439.
PF
XX
02-JUN-1999; 99WO-US012252.
PR
23-JUN-1999; 99US-0141037P.
PR
07-JUL-1999; 99US-0143048P.
PR
20-JUL-1999; 99US-0144758P.
PR
26-JUL-1999; 99US-0145698P.
PR
28-JUL-1999; 99US-0146222P.
PR
17-AUG-1999; 99US-0149396P.
PR
15-SEP-1999; 99WO-US021090.
PR
15-SEP-1999; 99WO-US021547.
PR
08-OCT-1999; 99US-0158663P.
PR
01-DEC-1999; 99WO-US028313.
PR
16-DEC-1999; 99WO-US030095.
PR
20-DEC-1999; 99WO-US030911.
PR
05-JAN-2000; 2000WO-US000219.
PR
06-JAN-2000; 2000WO-US000376.
PR
11-FEB-2000; 2000WO-US003565.
PR
22-FEB-2000; 2000WO-US004414.
PR
24-FEB-2000; 2000WO-US004914.
PR
24-FEB-2000; 2000WO-US005004.
PR
02-MAR-2000; 2000WO-US005841.
PR
15-MAR-2000; 2000WO-US006884.
PR
20-MAR-2000; 2000WO-US007377.
XX
(GETH ) GENENTECH INC.
XX
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI
Ferrara N, Fong S, Gerber H, Gerrieten ME, Goddard A, Godowski PJ;
PI
Grimaldi CJ, Gurney AL, Kijavini JJ, Napier MA, Pan J, Paoni NF;
PI
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI
Zhang Z;
XX
WPI; 2001-032160/04.
DR
```

DR P-PSDB; AAB65260.  
XX PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
PT to cause targeted cell death.  
XX Claim 2; Fig 249; 935pp; English.  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can  
CC be used for targeted delivery of bioactive molecules, such as toxins,  
CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
CC DNA. They may also be used to produce transgenic animals which are used  
CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
CC and protein sequence can be used for tissue typing and in treating  
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
CC AAF44470 represent PCR primers and hybridisation probes used in the  
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
CC AAB65300 represent human PRO polynucleotide and protein sequences given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;  
Query Match 98.7%; Score 1579.4; DB 5; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 20 CAGCCACAGACGGGTATGAGCGCGGTATATCTGCTGGCCCTCTCTGGGGTTATCTCTCC 79  
DB 1 CAGCCACAGACGGGTATGAGCGCGGTATATCTGCTGGCCCTCTCTGGGGTTATCTCTCC 60  
QY 80 ACTGCCAGGAGTGCAGCGCTCTCTGCCAGTTGGGACAGTTTCAGCATGTGTGGAGGT 139  
DB 61 ACTGCCAGGAGTGCAGCGCTCTCTGCCAGTTGGGACAGTTTCAGCATGTGTGGAGGT 120  
QY 140 GTCCGACCTGCCCGGCAATGGAACCCCTAAGAACACAGCTGCGACAGCGGCTTGGGGTG 199  
DB 121 GTCCGACCTACCCCGCAATGGACCCCTAAGAACACAGCTGCGACAGCGGCTTGGGGTG 180  
QY 200 CAGGACAGCTTGATGCTCAATTGAGAGCGGACCCCAAGTGAAGCTGCTCTCCAAAGG 259  
DB 181 CCAGGACAGCTTGATGCTCAATTGAGAGCGGACCCCAAGTGAAGCTGCTCTCCAAAGG 240  
QY 260 CTGACGGAGGCAAGGACAGAGCCCGCGTCACTGAGCACCCGATGGCCCGCCGCT 319  
DB 241 CTGACGGAGGCAAGGACAGAGCCCGCGTCACTGAGCACCCGATGGCCCGCCGCT 300  
QY 320 CTCCCTGATCTCTACACCTTCTGTGCGCGCCAGGAGGACTTCTGCAACAACTCGTTAA 379  
DB 301 CTCCCTGATCTCTACACCTTCTGTGCGCGCCAGGAGGACTTCTGCAACAACTCGTTAA 360  
QY 380 CTCCCTCCCGCTTGGGCGCCACAGCCCGCAGCAGACCCAGGATCTTGAAGTGCAGT 439  
DB 361 CTCCCTCCCGCTTGGGCGCCACAGCCCGCAGCAGACCCAGGATCTTGAAGTGCAGT 420  
QY 440 CTGCTTGTCTATGAGAGGCTCTGAGAGGGAACAACAGAGAGATCTGCCCCCAAGGGGAC 499  
DB 421 CTGCTTGTCTATGAGAGGCTCTGAGAGGGAACAACAGAGAGATCTGCCCCCAAGGGGAC 480  
QY 500 CACACACTGTATGATGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCAATCTGAG 559  
DB 481 CACACACTGTATGATGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCAATCTGAG 540  
QY 560 AGTCCAGGAGTATGCCCGCAGCCAGGTTGCAACTCTGATGGGACACAGGAATTTGG 619  
DB 541 AGTCCAGGAGTATGCCCGCAGCCAGGTTGCAACTCTGATGGGACACAGGAATTTGG 600  
QY 620 GCCCGTGGGTATGACATGAGAACTGCAATAGGAAGATTTCTGACCTGTCTCGGGGAC 679  
DB 601 GCCCGTGGGTATGACATGAGAACTGCAATAGGAAGATTTCTGACCTGTCTCGGGGAC 660

QY 680 CACCATTATGACACACCGGAACTTGGCTCAAGAACCCACTGATTTGGACCACTCGAATAC 739  
DB 661 CACCATTATGACACACCGGAACTTGGCTCAAGAACCCACTGATTTGGACCACTCGAATAC 720  
QY 740 CGAGATGTCGAGGTGGGCGAGTGTTCAGAGAGCGTGTCTCATAGATGATAGACT 799  
DB 721 CGAGATGTCGAGGTGGGCGAGTGTTCAGAGAGCGTGTCTCATAGATGATAGACT 780  
QY 800 CACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGCTCAAAAATCCCGAA 859  
DB 781 CACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGCTCAAAAATCCCGAA 840  
QY 860 GACCACCATTCACACTCAGCCCTCTCTGGGGTGTCTTGTGGCTCTCTATACCACTTCTGCTC 919  
DB 841 GACCACCATTCACACTCAGCCCTCTCTGGGGTGTCTTGTGGCTCTCTATACCACTTCTGCTC 900  
QY 920 CTGCGACCTGTGCAATAGTGCAGCAGCAGCAGCTTCTGCTGAATCTCCCTCTCTCTCA 979  
DB 901 CTGCGACCTGTGCAATAGTGCAGCAGCAGCAGCTTCTGCTGAATCTCCCTCTCTCTCA 960  
QY 980 AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTCTGCTGTGACGCCCTTGGAACTCTG 1039  
DB 961 AGCTGCCCTGTCTCCAGGAGACCGGAGTGTCTTCTGCTGTGACGCCCTTGGAACTCTG 1020  
QY 1040 TTCAAGTGGCTCTCCCTCCGAATGACCTGCCCCAGGGCGCCACTCATTTGTATGATGGTA 1099  
DB 1021 TTCAAGTGGCTCTCCCTCCGAATGACCTGCCCCAGGGCGCCACTCATTTGTATGATGGTA 1080  
QY 1100 GATTATCTCTCAGAGGTGGGCTGTCCACCAAAATGACATTCAGGCTGTGGTGGCCCA 1159  
DB 1081 GATTATCTCTCAGAGGTGGGCTGTCCACCAAAATGACATTCAGGCTGTGGTGGCCCA 1140  
QY 1160 ACCTTCCAGCTTCTTGTGTAACCAACACAGACAAATCGGGATCTTCTCTCGCGGTGAGAA 1219  
DB 1141 ACCTTCCAGCTTCTTGTGTAACCAACACAGACAAATCGGGATCTTCTCTCGCGGTGAGAA 1200  
QY 1220 GCGTGAATGTCAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTTGGAGTC 1279  
DB 1201 GCGTGAATGTCAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTTGGAGTC 1260  
QY 1280 TCTCACTGGGGGTGGGCTGGCACTGGCCCCAGGGCTGTGGTGGGGAGTGGTTGCC 1339  
DB 1261 TCTCACTGGGGGTGGGCTGGCACTGGCCCCAGGGCTGTGGTGGGGAGTGGTTGCC 1320  
QY 1340 TTCTCTGTAACCTTATTACCCCAAGATCTTTCACCGCTGCTGACCAACCACTCAACC 1399  
DB 1321 TTCTCTGTAACCTTATTACCCCAAGATCTTTCACCGCTGCTGACCAACCACTCAACC 1380  
QY 1400 TCCCTCTGACCTTCAACCTAATGCGCTTGGACACAGATTTCTTCCCAATTTCTGTCATG 1459  
DB 1381 TCCCTCTGACCTTCAACCTAATGCGCTTGGACACAGATTTCTTCCCAATTTCTGTCATG 1440  
QY 1460 AATCATCTTCCCAACACAAATTCATATCTATCTACCTTAACAGACACACTGGGGAGA 1519  
DB 1441 AATCATCTTCCCAACACAAATTCATATCTATCTACCTTAACAGACACACTGGGGAGA 1500  
QY 1520 GCTTGAGCATCGGACTTGGCTTGGAGAGGGGACCGCTGAGGAGTGGCTGCAATGTA 1579  
DB 1501 GCTTGAGCATCGGACTTGGCTTGGAGAGGGGACCGCTGAGGAGTGGCTGCAATGTA 1560  
QY 1580 TCTGATAATACAGCCCTGTC 1600  
DB 1561 TCTGATAATACAGCCCTGTC 1581

RESULT 11  
ABK33616  
ID ABK33616 standard; cDNA; 1587 BP.  
XX  
AC ABK33616;  
XX  
DT 08-MAY-2002 (first entry)  
XX



cdNA encoding human PRO protein, Seq ID No 161.

Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.

Homo sapiens.

WO200208288-A2.

31-JAN-2002.

29-JUN-2001; 2001WO-US021066.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220585P.

25-JUL-2000; 2000US-0220605P.

25-JUL-2000; 2000US-0220607P.

25-JUL-2000; 2000US-0220624P.

25-JUL-2000; 2000US-0220638P.

25-JUL-2000; 2000US-0220664P.

25-JUL-2000; 2000US-0220666P.

26-JUL-2000; 2000US-0220893P.

28-JUL-2000; 2000WO-US020710.

01-AUG-2000; 2000US-0222425P.

22-AUG-2000; 2000US-0227133P.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

10-NOV-2000; 2000WO-US030873.

28-NOV-2000; 2000US-0253646P.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006666.

22-MAR-2001; 2001US-00816744.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001WO-US017092.

(GETH ) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

WPI; 2002-172001/22.  
P-PSDB; AAU83672.

One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.

Claim 2; Fig 161; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumors, especially lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO protein coding sequences of the invention

SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 6; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGCCACAGACGGGTGATGAGCGGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCCC 79  
DB 1 CAGCCACAGACGGGTGATGAGCGGGTATTACTGTGGCCCTCTCTGGGGTTTCATCTCCC 60

QY 80 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGAAGGT 139  
DB 61 ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGAAGGT 120

QY 140 GTCCGACCTGCCCGGCAATGGACCCCTAAGAACACAGCTGGGACAGCGGCTTGGGGTG 199  
DB 121 GTCCGACCTACCCCGGCAATGGACCCCTAAGAACACAGCTGGGACAGCGGCTTGGGGTG 180

QY 200 CCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAAGTGTGTCTCTCAAGGG 259  
DB 181 CCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAAGTGTGTCTCTCAAGGG 240

QY 260 CTGCACGGAGGCAAGGACAGGAGCCCGCGCTCACTGAGCACCGGATGGGCCCCGGCCT 319  
DB 241 CTGCACGGAGGCAAGGACAGGAGCCCGCGCTCACTGAGCACCGGATGGGCCCCGGCCT 300

QY 320 CTCCCTGATCTCTACACCTTCTGTGTCGCGCAGGAGGACTTCTGCAACACCTCGTTAA 379  
DB 301 CTCCCTGATCTCTACACCTTCTGTGTCGCGCAGGAGGACTTCTGCAACACCTCGTTAA 360

QY 380 CTCCCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTTGAGGTCCCAGT 439  
DB 361 CTCCCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCTTTGAGGTCCCAGT 420

QY 440 CTGCTTTGTCTATGGAAGGCTGTCTGAGAGGGGCAACAAGAGAGATCTGCCCCAAGGGGAC 499  
DB 421 CTGCTTTGTCTATGGAAGGCTGTCTGAGAGGGGCAACAAGAGAGATCTGCCCCAAGGGGAC 480

QY 500 CACACACTGTTATGATGGGCTCTCTCAGGCTCAGGGAGGAGGAGGATCTTCCCAATCTGAG 559  
DB 481 CACACACTGTTATGATGGGCTCTCTCAGGCTCAGGGAGGAGGAGGATCTTCCCAATCTGAG 540

QY 560 AGTCCAGGAGTGCATGCCAGCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTTGG 619  
DB 541 AGTCCAGGAGTGCATGCCAGCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTTGG 600

QY 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 679  
DB 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 660

QY 680 CACCATTTGACACACGGAAACTTGGCTCAGAACCCACTGATTTGGACCATCGAATAC 739  
DB 661 CACCATTTGACACACGGAAACTTGGCTCAGAACCCACTGATTTGGACCATCGAATAC 720

QY 740 CGAGATGTCGAGGTGGGCGAGGTGTCTCAGGAGAGCGTCTGCTCATAGATGTAGGACT 799  
DB 721 CGAGATGTCGAGGTGGGCGAGGTGTCTCAGGAGAGCGTCTGCTCATAGATGTAGGACT 780

QY 800 CACATCAACCTCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTTCCCAAGAA 859  
DB 781 CACATCAACCTCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATTTCCCAAGAA 840

QY 860 GACCACATCCACTCAGCCCCCTCTCTGGGGTGTGTGGGCTCTCTATACCACCTTCTGCTC 919  
DB 841 GACCACATCCACTCAGCCCCCTCTCTGGGGTGTGTGGGCTCTCTATACCACCTTCTGCTC 900

QY 920 CTCGGACCTGTGCAATAGTGCAGGACGACGCGTTCTGCTGAACCTCCCTCCCTCTCA 979  
DB 901 CTCGGACCTGTGCAATAGTGCAGGACGACGCGTTCTGCTGAACCTCCCTCCCTCTCA 960

QY 980 AGCTGCCCTCTGTCCCAGGAGACCGGCGAGTGTCTTACCTGTGTGTCAGGCCCCCTTGGAACTG 1039  
DB 961 AGCTGCCCTCTGTCCCAGGAGACCGGCGAGTGTCTTACCTGTGTGTCAGGCCCCCTTGGAACTG 1020



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QY 1040 TTCAAGTGGTCTCCCGGATGACCTCGCCCGAGGGCGGCACCTCATTTGTTATGATGGGTA 1099
|
|
|
Db 1021 TTCAAGTGGTCTCCCGGATGACCTCGCCCGAGGGCGGCACCTCATTTGTTATGATGGGTA 1080
|
|
|
QY 1100 CATTCATCTCTCAGGAGGTGGGTGTCACCAAAATGAGCATTTACAGGGCTGCGTGCCCA 1159
|
|
|
Db 1081 CATTCATCTCTCAGGAGGTGGGTGTCACCAAAATGAGCATTTACAGGGCTGCGTGCCCA 1140
|
|
|
QY 1160 ACCTTCAGCTCTCTGTTGAACACACACAGCAAAATCGGGATCTTCTCTGCGCGTGAGAA 1219
|
|
|
Db 1141 ACCTTCAGCTCTCTGTTGAACACACACAGCAAAATCGGGATCTTCTCTGCGCGTGAGAA 1200
|
|
|
QY 1220 GCGTGATGTGACGCTCTCGCTCTCAGCATGAGGAGGTGGGGCTGAGGGCTGAGATC 1279
|
|
|
Db 1201 GCGTGATGTGACGCTCTCGCTCTCAGCATGAGGAGGTGGGGCTGAGGGCTGAGATC 1260
|
|
|
QY 1280 TCTCACTTGGGGGTGGGGCTGACATGCGCCCGAGCGCTGTGTGGTGGGAGTGTGTTGCC 1339
|
|
|
Db 1261 TCTCACTTGGGGGTGGGGCTGACATGCGCCCGAGCGCTGTGTGGTGGGAGTGTGTTGCC 1320
|
|
|
QY 1340 TTCTCTGTAACCTATTACCCCGACGATTTCTTCAACGCTGCTGACACCCACACTCAAC 1399
|
|
|
Db 1321 TTCTCTGTAACCTATTACCCCGACGATTTCTTCAACGCTGCTGACACCCACACTCAAC 1380
|
|
|
QY 1400 TCCTCTGACCTCATTAACCTTAATGGCTTGGACACAGATTTCTTCCCATTTCTGTCCATG 1459
|
|
|
Db 1381 TCCTCTGACCTCATTAACCTTAATGGCTTGGACACAGATTTCTTCCCATTTCTGTCCATG 1440
|
|
|
QY 1460 AATCATTTCCCGACACACAAATCATTTACTTACTTACCTTAACAGCAACACTGGGGAGA 1519
|
|
|
Db 1441 AATCATTTCCCGACACACAAATCATTTACTTACTTACCTTAACAGCAACACTGGGGAGA 1500
|
|
|
QY 1520 GCTGTGAGCATCGGACTTGCCTATGGGAGGGGACGCTGGAGAGTGGCTGCATGTA 1579
|
|
|
Db 1501 GCTGTGAGCATCGGACTTGCCTATGGGAGGGGACGCTGGAGAGTGGCTGCATGTA 1560
|
|
|
QY 1580 TCTGATAATACAGACCTGTGTC 1600
|
|
|
Db 1561 TCTGATAATACAGACCTGTGTC 1581
|
|
|
RESULT 12
ID ABS68390
AC ABS68390 standard; cDNA; 1587 BP.
AC ABS68390;
XX
XX
DT 18-NOV-2002 (first entry)
XX
DE Human cDNA encoding secreted protein PRO1863.
XX
KW Human; sg; gene; secreted and transmembrane protein; PRO1800; PRO539;
KW PRO982; PRO1434; PRO1863; PRO1917; PRO1868; PRO3434;
KW inflammatory disorder; immune related disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW psoriasis; allergic disease of the lung; graft-versus host disease;
KW tumour; gene therapy.
XX
XX Homo sapiens.
XX
XX US2002098506-A1.
XX
XX 25-JUL-2002.
XX
XX 27-DEC-2001; 2001US-00033301.
XX
XX 04-AUG-1998; 98US-0095325P.
XX 16-DEC-1998; 98US-0112851P.
XX 16-DEC-1998; 98US-0113145P.
XX 22-DEC-1998; 98US-0113511P.
XX 12-JAN-1999; 99US-0115558P.
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PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
XX Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
XX Wood WI;
XX WPI; 2002-690475/74.
XX P-PSDB; ABG92707.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides useful
XX for diagnosis and treatment of inflammatory disorders and immune-related
XX diseases, and identifying modulators.
XX
XX Claim 2; Fig 9; 125pp; English.
XX
XX The invention relates to an isolated polypeptide having at least 80%
XX amino acid sequence identity to secreted and transmembrane polypeptides
XX PRO1800, PRO539, PRO1917, PRO1868, PRO3434 or
XX PRO1927 and their encoding nucleic acids. Also included are vectors, host
XX cells and antibodies against PRO polypeptides. PRO proteins are useful
XX for identifying modulators of the polypeptide. PRO1868 useful for the
XX diagnosis and treatment of inflammatory and immune related diseases
XX including systemic lupus erythematosus, rheumatoid arthritis, systemic
XX sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
XX infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
XX versus host disease and tumours. Pro nucleic acids are useful for
XX constructing hybridisation probes for mapping the gene that encodes that
XX PRO and for the genetic analysis of individuals with genetic disorders,
XX and for generating transgenic animals which are useful in the development
XX and screening of therapeutically useful reagents. PRO nucleic acids are
XX also useful for gene therapy, chromosome identification, and tissue
XX typing. PRO proteins are useful as molecular weight markers for protein
XX electrophoresis purposes. The anti-PRO antibodies are useful in
XX diagnostic assays for PRO, e.g. detecting its expression in specific
XX cells, tissues or serum and for affinity purification of PRO. The present
XX sequence encodes a PRO protein
XX
XX Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;
XX
XX Query Match 98.7%; Score 1579.4; DB 6; Length 1587;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 CAGCCACAGACGGGTCATGAGCGCGTATTACTGTGGCCCTCTCGGGGTTCATCTCCC 79
|
|
|
Db 1 CAGCCACAGACGGGTCATGAGCGCGTATTACTGTGGCCCTCTCGGGGTTCATCTCCC 60
|
|
|
QY 80 ACTGCCAGGAGTGCAGGCGCTCTCTGCCAGTTTGGACAGTTCAGCATGTGTGGAGGT 139
|
|
|
Db 61 ACTGCCAGGAGTGCAGGCGCTCTCTGCCAGTTTGGACAGTTCAGCATGTGTGGAGGT 120
|
|
|
QY 140 GTCCGACCTGCCCGGCAATGACCCCTAAGAACACACAGCTGGGACAGCGGCTGGGGTG 199
|
|
|
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Db 121 GTCGACCTACCCGGCAATGAGACCCCTAAGAAACACACAGCTGCGACAGCGCTTGGGGTG 180  
Qy 200 CAGGACAGCTTGTATGCTCATTTGAGAGCGAGACCCCAAGTGAAGCTGTCTCTCCAAAGG 259  
Db 181 CCAGGACAGCTTGTATGCTCATTTGAGAGCGAGACCCCAAGTGAAGCTGTCTCTCCAAAGG 240  
Qy 260 CTGACGGAGGCCAAAGGACCAAGGACCGCCCGCTCACTGAGCACCGGATGGGCCCGCCGCT 319  
Db 241 CTGACGGAGGCCAAAGGACCAAGGACCGCCCGCTCACTGAGCACCGGATGGGCCCGCCGCT 300  
Qy 320 CTCCTGTATCTCTTACACTTGTGTGTCGCCCAAGGAGGACTTCTGCAACAACTCGTTAA 379  
Db 301 CTCCTGTATCTCTTACACTTGTGTGTCGCCCAAGGAGGACTTCTGCAACAACTCGTTAA 360  
Qy 380 CTCCTCTCCGCTTGGGCCCAAGGACCGCCCGCTCACTGAGCACCGGATGGGCCCGCCGCT 439  
Db 361 CTCCTCTCCGCTTGGGCCCAAGGACCGCCCGCTCACTGAGCACCGGATGGGCCCGCCGCT 420  
Qy 440 CTGCTTGTCTATGGAAGGCTGTCTGAGGGGGAACAAGAGAGATCTGCCCAAGGGGAC 499  
Db 421 CTGCTTGTCTATGGAAGGCTGTCTGAGGGGGAACAAGAGAGATCTGCCCAAGGGGAC 480  
Qy 500 CACACTGTATATGAGGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCCAATCTGAG 559  
Db 481 CACACTGTATATGAGGCTCTCTCAGGCTCAGGGAGGAGGATCTTCTCCAATCTGAG 540  
Qy 560 AGTCCAGGATGATGCCCGCAGGCTTGCAGACCTGCTCAATGGGACACAGGAATGG 619  
Db 541 AGTCCAGGATGATGCCCGCAGGCTTGCAGACCTGCTCAATGGGACACAGGAATGG 600  
Qy 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 679  
Db 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 660  
Qy 680 CACCAATTATGACACACGAACTTGGCTCAAGAACCCCACTGATGGACACACATCGAATAC 739  
Db 661 CACCAATTATGACACACGAACTTGGCTCAAGAACCCCACTGATGGACACACATCGAATAC 720  
Qy 740 CGAGATGTGGAGTGGGGAGGTGTGTCTAGGAGACGCTGCTGCTCATAGATGAGGACT 799  
Db 721 CGAGATGTGGAGTGGGGAGGTGTGTCTAGGAGACGCTGCTGCTCATAGATGAGGACT 780  
Qy 800 CACATCAACCTGTGGGGACAAAGCTGCAGACCTGTTGGGGCTCAAAATTCACAGAA 859  
Db 781 CACATCAACCTGTGGGGACAAAGCTGCAGACCTGTTGGGGCTCAAAATTCACAGAA 840  
Qy 860 GACCACCATCTACTCAGCCCTCTCTGGGGTGTCTGTGGCTCTCTATACCCACTTCTGCTC 919  
Db 841 GACCACCATCTACTCAGCCCTCTCTGGGGTGTCTGTGGCTCTCTATACCCACTTCTGCTC 900  
Qy 920 CTCGGACCTGTGCAATAGTCCAGACGACGAGCGTGTCTGAACTCCCTCCCTCTCTCA 979  
Db 901 CTCGGACCTGTGCAATAGTCCAGACGACGAGCGTGTCTGAACTCCCTCCCTCTCTCA 960  
Qy 980 AGCTGCCCTGTCTCCAGGACCGGAGTGTCTTACCTGTGTGAGCGCCCTTGGAACCTG 1039  
Db 961 AGCTGCCCTGTCTCCAGGACCGGAGTGTCTTACCTGTGTGAGCGCCCTTGGAACCTG 1020  
Qy 1040 TTCAAGTGGCTCCCGCAATGACCTGCCCGAGGGGCGCACTCATTTGTTATGATGGGTA 1099  
Db 1021 TTCAAGTGGCTCCCGCAATGACCTGCCCGAGGGGCGCACTCATTTGTTATGATGGGTA 1080  
Qy 1100 CATTCATCTCTCAGGAGTGGGTGTCTCCACCAAAATGAGCAATTCAGGGCTGCGTGGCCCA 1159  
Db 1081 CATTCATCTCTCAGGAGTGGGTGTCTCCACCAAAATGAGCAATTCAGGGCTGCGTGGCCCA 1140  
Qy 1160 ACCTTCAGGCTCTCTGTAACCAACACCAAGGAGGATCTTCTCTCGCGGTGAGAA 1219  
Db 1141 ACCTTCAGGCTCTCTGTAACCAACACCAAGGAGGATCTTCTCTCGCGGTGAGAA 1200  
Qy 1220 GCCTGATGTGAGCCTCTCTGCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCTGAGGTC 1279  
Db 1201 GCCTGATGTGAGCCTCTCTGCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCTGAGGTC 1260

Qy 1280 TCTCACTTGGGGGTGGGGCTGGCACTGGCCCGACGCGCTGTGGTGGGAGTGGTTGCC 1339  
Db 1261 TCTCACTTGGGGGTGGGGCTGGCACTGGCCCGACGCGCTGTGGTGGGAGTGGTTGCC 1320  
Qy 1340 TTCTCTGTAACCTATTTACCCCCACGATTTCTTCAACGCTGTGACACCCACACTCAACC 1399  
Db 1321 TTCTCTGTAACCTATTTACCCCCACGATTTCTTCAACGCTGTGACACCCACACTCAACC 1380  
Qy 1400 TCCCTCTGACCTCATTAACCTAATGGCTTGGGACACGAGATTTCTTCCCATTTCTGTCATG 1459  
Db 1381 TCCCTCTGACCTCATTAACCTAATGGCTTGGGACACGAGATTTCTTCCCATTTCTGTCATG 1440  
Qy 1460 AATCATCTTCCCCACACACAAATCATTCATATCTACTTCACTTAACAGCAACTGGGGAGA 1519  
Db 1441 AATCATCTTCCCCACACACAAATCATTCATATCTACTTCACTTAACAGCAACTGGGGAGA 1500  
Qy 1520 GCCTGGAGCATCCGAGCTTGGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1579  
Db 1501 GCCTGGAGCATCCGAGCTTGGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTA 1560  
Qy 1580 TCTGATAATAACAGACCTGTGTC 1600  
Db 1561 TCTGATAATAACAGACCTGTGTC 1581

## RESULT 13

ABS67458

ID ABS67458 standard; cDNA; 1587 BP.

XX AC ABS67458;  
XX XT

DT 29-NOV-2002 (first entry)

XX cDNA encoding novel human secreted protein #5.

XX Human; secreted protein; transmembrane protein; gene mapping; transgenic;  
XX gene; ss.

XX Homo sapiens.

XX US2002098505-A1.

XX 25-JUL-2002.

XX 28-DEC-2001; 2001US-00033246.

XX 04-AUG-1998; 98US-0095325P.

XX 16-DEC-1998; 98US-0112851P.

XX 16-DEC-1998; 98US-0113145P.

XX 22-DEC-1998; 98US-0113511P.

XX 12-JAN-1999; 99US-0115558P.

XX 12-JAN-1999; 99US-0115565P.

XX 09-FEB-1999; 99US-0119341P.

XX 10-FEB-1999; 99US-0119537P.

XX 12-FEB-1999; 99US-0119965P.

XX 02-JUN-1999; 99WO-US012252.

XX 29-OCT-1999; 99US-0162506P.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 09-DEC-1999; 99US-0170262P.

XX 11-FEB-2000; 2000WO-US003565.

XX 22-FEB-2000; 2000WO-US004414.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 30-MAR-2000; 2000WO-US008439.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 01-DEC-2000; 2000WO-US032678.

XX 25-MAY-2001; 2001US-00866034.

XX (GETH ) GENENTECH INC.

XX Botstein D, Desnovers L, Ferrara N, Fong S, Gao W, Goddard A;  
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;  
PI Wood WI;  
XX WPI; 2002-665999/71.  
DR P-PSDB; ABG91359.  
XX New human secreted and transmembrane (PRO) polypeptides, useful for  
PT treating conditions requiring PRO polypeptides, for screening PRO  
PT antagonists and agonists useful as drug candidates.  
XX Claim 2; Fig 9; 125pp; English.  
XX The invention relates to new human secreted and transmembrane proteins  
CC (PRO) and nucleic acids of the invention. The polypeptides can be  
CC administered therapeutically, especially by expressing encoding  
CC polynucleotides, e.g. in therapeutic compositions. They can be used to  
CC screen for PRO polypeptide antagonists and agonists useful to identify  
CC drug candidates. They can also be used to produce antibodies, useful to  
CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or  
CC therapeutically (e.g. as antagonists or to target and/or deliver  
CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to  
CC produce antisense sequences to inhibit polypeptide production. They can  
CC be used to produce probes and primers useful to detect or isolate  
CC sequences encoding PRO polypeptides or similar sequences e.g. variants or  
CC sequences from other species. They are also useful for gene mapping and  
CC to generate transgenic animals. ABS67448-ABS67476 represent human PRO  
CC coding sequences, probes and primers of the invention  
XX Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;  
SQ  
Query Match 98.7%; Score 1579.4; DB 6; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 20 CAGCCACAGACGGGTATGAGCGCGTATTACTGTGGCCCTCCTGGGGTTATCCTCCC 79  
DB 1 CAGCCACAGACGGGTATGAGCGCGTATTACTGTGGCCCTCCTGGGGTTATCCTCCC 60  
QY 80 ACTGCCAGGAGTCAGGCGCTGCTCCAGTTGGGACAGTTTCACATGCTGGAGCT 139  
DB 61 ACTGCCAGGAGTCAGGCGCTGCTCCAGTTGGGACAGTTTCACATGCTGGAGCT 120  
QY 140 GTCCGACCTGCCCGGCAATGACCCCTAAGAACACACAGCTGGCAGCGGCTTGGGGTG 199  
DB 121 GTCCGACCTACCCCGCAATGGACCCCTAAGAACACACAGCTGGCAGCGGCTTGGGGTG 180  
QY 200 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCTTGGTCTCCAAAGG 259  
DB 181 CCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCTTGGTCTCCAAAGG 240  
QY 260 CTGACGAGGAGCCAAAGACAGAGCCCGCGTCACTGAGCACCAGTGGCCCGGCGCT 319  
DB 241 CTGACGAGGAGCCAAAGACAGAGCCCGCGTCACTGAGCACCAGTGGCCCGGCGCT 300  
QY 320 CTCCTCTGATCTCTACACCTTCTGTGTGCCAGGAGGACTTCGCAACACCTCGTTAA 379  
DB 301 CTCCTCTGATCTCTACACCTTCTGTGTGCCAGGAGGACTTCGCAACACCTCGTTAA 360  
QY 380 CTCCTCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGGAGTGGCCAGT 439  
DB 361 CTCCTCTCCGCTTTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGGAGTGGCCAGT 420  
QY 440 CTGCTTGTCTATGGAAGGCTCTGAGGGGCAACAGAGAGATCTGCCCCCAAGGGGAC 499  
DB 421 CTGCTTGTCTATGGAAGGCTCTGAGGGGCAACAGAGAGATCTGCCCCCAAGGGGAC 480  
QY 500 CACACACTGTTATGATGGCTCCTCAGGCTCAGGGGAGGAGGATCTTCTCCAACTGAG 559  
DB 481 CACACACTGTTATGATGGCTCCTCAGGCTCAGGGGAGGAGGATCTTCTCCAACTGAG 540  
QY 560 AGTCCAGGAGTGCATGCCCCCAGCAGGTTGCCAACCTGCTCAATGGGACACAGGAATGG 619

DB 541 AGTCCAGGAGTGCATGCCCCCAGCAGGTTGCCAACCTGCTCAATGGGACACAGGAATGG 600  
QY 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTCTGACCTGTCTATCGGGGAC 679  
DB 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAAGATTTCTGACCTGTCTATCGGGGAC 660  
QY 680 CACCATTATGACACACGGAACCTTGGCTCAAGAACCCACTGATTTGGACACACATCGAATAC 739  
DB 661 CACCATTATGACACACGGAACCTTGGCTCAAGAACCCACTGATTTGGACACACATCGAATAC 720  
QY 740 CGAGATGTCGAGGTGGGCGAGGTGTCTCAGAGACGCTGCTCTATAGATAGTAGACT 799  
DB 721 CGAGATGTCGAGGTGGGCGAGGTGTCTCAGAGACGCTGCTCTATAGATAGTAGACT 780  
QY 800 CACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATCCAGAA 859  
DB 781 CACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGTTGGGGCTCAAAATCCAGAA 840  
QY 860 GACCACCATCCACTCAGCCCCCTCCTGGGGTGTCTTGTGGCTCCTATACCCACTTCTGCTC 919  
DB 841 GACCACCATCCACTCAGCCCCCTCCTGGGGTGTCTTGTGGCTCCTATACCCACTTCTGCTC 900  
QY 920 CTGCGACCTGTGCAATAGTGCAGAGACGAGCGTTCTGCTGAACCTCCCTCCCTCTCA 979  
DB 901 CTGCGACCTGTGCAATAGTGCAGAGACGAGCGTTCTGCTGAACCTCCCTCCCTCTCA 960  
QY 980 AGCTGCCCTGTGCCAGGAGACCGGCGAGTGTCTACTGTGTGCAGCCCCCTTGGAACTG 1039  
DB 961 AGCTGCCCTGTGCCAGGAGACCGGCGAGTGTCTACTGTGTGCAGCCCCCTTGGAACTG 1020  
QY 1040 TTCAAGTGTGCTCCCCCGAATGACCTGCCCGGAGGCGCCACTCATTTGTTATGATGGTA 1099  
DB 1021 TTCAAGTGTGCTCCCCCGAATGACCTGCCCGGAGGCGCCACTCATTTGTTATGATGGTA 1080  
QY 1100 CATTATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1159  
DB 1081 CATTATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCA 1140  
QY 1160 ACCTTCCAGCTTCTTGTGTAACACACACAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1219  
DB 1141 ACCTTCCAGCTTCTTGTGTAACACACACAGACAAATCGGGATCTTCTCTGCGCGTGAGAA 1200  
QY 1220 GCGTATGTCAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTGAGGTC 1279  
DB 1201 GCGTATGTCAGCTCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCTGAGGTC 1260  
QY 1280 TCTCAGTTGGGGGTGGGCTGGCACTGGCCCCCAGCGCTGTGTGGGGAGTGGTTGGCC 1339  
DB 1261 TCTCAGTTGGGGGTGGGCTGGCACTGGCCCCCAGCGCTGTGTGGGGAGTGGTTGGCC 1320  
QY 1340 TTCTGCTAACTCTATTACCCCCCAGATTCTTCAACCGCTGTGACCAACCCACACTCAACC 1399  
DB 1321 TTCTGCTAACTCTATTACCCCCCAGATTCTTCAACCGCTGTGACCAACCCACACTCAACC 1380  
QY 1400 TCCCTCTGACCTCATAACCTAATGGCTTGGACAACAGATTCTTTCCATTTCTGTCATG 1459  
DB 1381 TCCCTCTGACCTCATAACCTAATGGCTTGGACAACAGATTCTTTCCATTTCTGTCATG 1440  
QY 1460 AATCATCTTCCCAACACACATCATATCTACTCACTCACTAACACACACACTGGGGAGA 1519  
DB 1441 AATCATCTTCCCAACACACATCATATCTACTCACTCACTAACACACACACTGGGGAGA 1500  
QY 1520 GCTTGAGCATCCGAGCTTGGCCCTATGGGAGGGGACGCTGAGGAGTGGCTGCTATGTA 1579  
DB 1501 GCTTGAGCATCCGAGCTTGGCCCTATGGGAGGGGACGCTGAGGAGTGGCTGCTATGTA 1560  
QY 1580 TCTGATAATACAGCCCTGTC 1600  
DB 1561 TCTGATAATACAGCCCTGTC 1581

ABSS3475  
 ID ABS53475 standard; cDNA; 1587 BP.  
 XX  
 AC ABS53475;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE cDNA encoding human PRO1863 polypeptide.  
 XX  
 KW Human; secreted and transmembrane polypeptide; PRO polypeptide;  
 KW T-lymphocyte proliferation; inflammatory disease; rheumatoid arthritis;  
 KW inflammatory bowel disease; Sjogren's syndrome; thyroiditis;  
 KW autoimmune haemolytic anaemia; diabetes mellitus; multiple sclerosis;  
 KW hepatitis; contact dermatitis; allergic disease; psoriasis; virucide;  
 KW immune related disease; kidney disease; antiinflammatory; antithyroid;  
 KW antirheumatic; antiarthritic; immunosuppressive; antianaemic;  
 KW antidiabetic; neuroprotective; hepatotropic; antiinflammatory;  
 KW dermatological; antiallergic; antipsoriatic; PRO1863; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 17..1330  
 FT /\*tag= a  
 FT /product= "PRO1863"  
 XX  
 US2002098507-A1.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 27-DEC-2001; 2001US-00033326.  
 XX  
 PR 04-AUG-1998; 98US-0095325P.  
 PR 16-DEC-1998; 98US-0112851P.  
 PR 16-DEC-1998; 98US-0113145P.  
 PR 22-DEC-1998; 98US-0113511P.  
 PR 12-JAN-1999; 99US-0115558P.  
 PR 12-JAN-1999; 99US-0115565P.  
 PR 12-JAN-1999; 99US-0115733P.  
 PR 09-FEB-1999; 99US-0119341P.  
 PR 10-FEB-1999; 99US-0119537P.  
 PR 12-FEB-1999; 99US-0119565P.  
 PR 02-JUN-1999; 99US-012252.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 01-DEC-1999; 99US-028634.  
 PR 02-DEC-1999; 99US-028651.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 11-FEB-2000; 2000US-0003565.  
 PR 22-FEB-2000; 2000US-0004414.  
 PR 02-MAR-2000; 2000US-0005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 30-MAR-2000; 2000US-0008439.  
 PR 30-MAY-2000; 2000US-0014941.  
 PR 02-JUN-2000; 2000US-0015264.  
 PR 01-DEC-2000; 2000US-0032678.  
 PR 25-MAY-2001; 2001US-00866034.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;  
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 DR WPI; 2002-673823/72.  
 DR P-PSDB; ABG31399.  
 XX  
 XX Novel PRO polypeptides and nucleic acids encoding the polypeptides,  
 PT useful for preparing a medicament for the treatment of inflammatory and  
 PT immune related disorders.  
 XX  
 PS Claim 2; Fig 9; 125pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human secreted

CC and transmembrane polypeptides, designated PRO polypeptides, and the  
 CC polynucleotide sequences encoding them. The PRO polypeptides of the  
 CC invention include PRO1800, PRO539, PRO1834, PRO1863, PRO1917,  
 CC PRO1868, PRO3434 and PRO1927. The PRO polypeptides can inhibit the  
 CC stimulation of T-lymphocyte proliferation. The PRO polypeptides are  
 CC useful for the diagnosis and treatment of inflammatory diseases (e.g.  
 CC inflammatory bowel disease, rheumatoid arthritis, Sjogren's syndrome,  
 CC autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus, multiple  
 CC sclerosis, hepatitis, contact dermatitis, allergic diseases and  
 CC psoriasis), immune related diseases, and kidney diseases in humans. The  
 CC present sequence encodes human PRO1863 polypeptide  
 XX  
 SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;  
 Query Match 98.7%; Score 1579.4; DB 6; Length 1587;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 20 CAGCCACAGACGGGTCTATGAGCGCGGTATTACTGTGGCCCTCTCTGGGGTTCATCTCTCCC 79  
 DB 1 CAGCCACAGACGGGTCTATGAGCGCGGTATTACTGTGGCCCTCTCTGGGGTTCATCTCTCCC 60  
 QY 80 ACTGCCAGGAGTGCAGCGCTGCTCTGCCAGTTTGGACAGTTGAGCATGTGTGAAGGT 139  
 DB 61 ACTGCCAGGAGTGCAGCGCTGCTCTGCCAGTTTGGACAGTTTGGACAGTTGTGAAGGT 120  
 QY 140 GTCCGACCTGCCCGGCAATGGACCCCTAAGAACACCAGCTGGACAGCGCTTGGGGTG 199  
 DB 121 GTCCGACCTGCCCGGCAATGGACCCCTAAGAACACCAGCTGGACAGCGCTTGGGGTG 180  
 QY 200 CCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTAGGCTGTGTCTCTCAAGGG 259  
 DB 181 CCAGGACACGTTGATGCTCATTTGAGAGCGGACCCCAAGTAGGCTGTGTCTCTCAAGGG 240  
 QY 260 CTGCACGGAGGCCAAGAACCCAGAGCCCGCTGCTCTGACGACCGGATGGGCCCCGGCT 319  
 DB 241 CTGCACGGAGGCCAAGAACCCAGAGCCCGCTGCTCTGACGACCGGATGGGCCCCGGCT 300  
 QY 320 CTCCCTGATCTCTCACCTTCTGTGTGTCGCCAGGAGGACTTCTGCAACACCTCTGTTAA 379  
 DB 301 CTCCCTGATCTCTCACCTTCTGTGTGTCGCCAGGAGGACTTCTGCAACACCTCTGTTAA 360  
 QY 380 CTCCCTCCCGCTTTGGGCCCCCAGAGCCCGCAGACCCAGGATCTCTTGAAGTCCCGCAGT 439  
 DB 361 CTCCCTCCCGCTTTGGGCCCCCAGAGCCCGCAGACCCAGGATCTCTTGAAGTCCCGCAGT 420  
 QY 440 CTGCTTGTCTATGGAAGGTGCTCTGAGAGGGGCAACAGAGAGATCTGCCCCAAGGGGAC 499  
 DB 421 CTGCTTGTCTATGGAAGGTGCTCTGAGAGGGGCAACAGAGAGATCTGCCCCAAGGGGAC 480  
 QY 500 CACACACTGTATGATGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCATCTGAG 559  
 DB 481 CACACACTGTATGATGGCTCTCTCAGGCTCAGGGGAGGAGGATCTTCTCCATCTGAG 540  
 QY 560 AGTCCAGGAGTGCATGCCCGCAGCGAGTTGCAACCTGCTCAATGGGACACAGAAATGG 619  
 DB 541 AGTCCAGGAGTGCATGCCCGCAGCGAGTTGCAACCTGCTCAATGGGACACAGAAATGG 600  
 QY 620 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 679  
 DB 601 GCCCGTGGGTATGACTGAGAACTGCAATAGGAAGATTTTCTGACCTGTCTATCGGGGAC 660  
 QY 680 CACCATTTGACACACGGAACTTGGCTCAAGAACCCACTGATTGGACCATCATGATAC 739  
 DB 661 CACCATTTGACACACGGAACTTGGCTCAAGAACCCACTGATTGGACCATCATGATAC 720  
 QY 740 CGAGATGTGGAGTGGGGCAGGTGTGTCTCAGGAGACGCTGCTCTATAGTAGTACT 799  
 DB 721 CGAGATGTGGAGTGGGGCAGGTGTGTCTCAGGAGACGCTGCTCTATAGTAGTACT 780  
 QY 800 CACATCAACCTCGTGGGGACAAAGGCTGACAGCTGTGGGGCTCAAAATTTCCAGAA 859  
 DB 781 CACATCAACCTCGTGGGGACAAAGGCTGACAGCTGTGGGGCTCAAAATTTCCAGAA 840

QY	860	GACCACATCCACTCAGCCCTCCTGGGTGCTTGTGGCTCTCTATACCACTTCTGCTC	919	XX
Db	841	GACCACATCCACTCAGCCCTCCTGGGTGCTTGTGGCTCTCTATACCACTTCTGCTC	900	XX
QY	920	CTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCAGCTTCTGTGAATCCCTCCCTCA	979	PR
Db	901	CTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCAGCTTCTGTGAATCCCTCCCTCA	960	PR
QY	980	AGCTGCCCTGTCTCCAGGAGACGGCAGTGTCTACTCTGTGTGACGCCCTTGGACCTG	1039	PR
Db	961	AGCTGCCCTGTCTCCAGGAGACGGCAGTGTCTACTCTGTGTGACGCCCTTGGACCTG	1020	PR
QY	1040	TTCAAGTGGCTCCCCCGCAATGACCTGACCTGCCCGGGCGCCACTCATTTATGATGGTA	1099	PR
Db	1021	TTCAAGTGGCTCCCCCGCAATGACCTGCCCGGGCGCCACTCATTTATGATGGTA	1080	PR
QY	1100	CATTTCATCTCTAGGAGGTGGCTGTCCACCAAAATGAGCATTCAGGGCTGGTGGCCCA	1159	PR
Db	1081	CATTTCATCTCTAGGAGGTGGCTGTCCACCAAAATGAGCATTCAGGGCTGGTGGCCCA	1140	PR
QY	1160	ACCTTCCAGCTTCTGTGAAACACACACAGCAAAATCGGGATCTTCTGCGCGTGAGAA	1219	PR
Db	1141	ACCTTCCAGCTTCTGTGAAACACACACAGCAAAATCGGGATCTTCTGCGCGTGAGAA	1200	PR
QY	1220	GGTGATGTGACGCTCTCTGCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCTGGAGTC	1279	PR
Db	1201	GGTGATGTGACGCTCTCTGCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCTGGAGTC	1260	PR
QY	1280	TCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGTGGGGAGTGTGTTGCC	1339	PR
Db	1261	TCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGTGGGGAGTGTGTTGCC	1320	PR
QY	1340	TTCTCTGCTAACTTCTATTACCCCAACGATTTCTTCCCGCTGTGACCAACCACTCAAC	1399	PR
Db	1321	TTCTCTGCTAACTTCTATTACCCCAACGATTTCTTCCCGCTGTGACCAACCACTCAAC	1380	PR
QY	1400	TCCTCTGACCTCATACCTAATGGCTTGGACACAGAGTTCTTCCCATCTTGTCCATG	1459	PR
Db	1381	TCCTCTGACCTCATACCTAATGGCTTGGACACAGAGTTCTTCCCATCTTGTCCATG	1440	PR
QY	1460	AATCATCTTCCACACACAAATCATATCTACTACTACTTAACAGCAACACTGGGGAGA	1519	PR
Db	1441	AATCATCTTCCACACACAAATCATATCTACTACTACTTAACAGCAACACTGGGGAGA	1500	PR
QY	1520	GCTTGAGCATCGGACTTGCCTATGGGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1579	PR
Db	1501	GCTTGAGCATCGGACTTGCCTATGGGAGGGGACGCTGGAGGAGTGGCTGCATGTA	1560	PR
QY	1580	TCTGATAATACAGACCTGTGTC	1600	PR
Db	1561	TCTGATAATACAGACCTGTGTC	1581	PR
RESULT 15				
ID	ADY31901	standard; cDNA; 1587 BP.		
XX				
AC	ADY31901;			
XX				
DT	05-MAY-2005	(first entry)		
DE				
DE		Novel human secreted and transmembrane protein PRO1181 cDNA.		
KW		PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; tumour;		
KW		cancer; lung; colon; breast; prostate; rectum; liver;		
KW		tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;		
KW		pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;		
OS		arthritis; sports injury; cytostatic; antiarthritic.		
XX				
OS		Homo sapiens.		
XX				
PN		WO200193983-A1.		

XX	13-DEC-2001.			
XX				
PF	01-JUN-2001; 2001WO-US017800.			
XX				
PR	02-JUN-2000; 2000WO-US015264.			
PR	05-JUN-2000; 2000US-0209832P.			
PR	20-JUN-2000; 2000US-0212901P.			
PR	22-JUN-2000; 2000US-0213807P.			
PR	20-JUL-2000; 2000US-0219556P.			
PR	25-JUL-2000; 2000US-0220585P.			
PR	25-JUL-2000; 2000US-0220603P.			
PR	25-JUL-2000; 2000US-0220624P.			
PR	25-JUL-2000; 2000US-0220638P.			
PR	25-JUL-2000; 2000US-0220664P.			
PR	25-JUL-2000; 2000US-0220666P.			
PR	26-JUL-2000; 2000US-0220893P.			
PR	28-JUL-2000; 2000WO-US020710.			
PR	01-AUG-2000; 2000US-0222425P.			
PR	22-AUG-2000; 2000US-0227133P.			
PR	23-AUG-2000; 2000WO-US023522.			
PR	24-AUG-2000; 2000WO-US023328.			
PR	10-NOV-2000; 2000WO-US030873.			
PR	28-NOV-2000; 2000US-0253646P.			
PR	01-DEC-2000; 2000WO-US032678.			
PR	20-DEC-2000; 2000US-00747259.			
PR	20-DEC-2000; 2000WO-US034956.			
PR	28-FEB-2001; 2001WO-US006520.			
PR	01-MAR-2001; 2001WO-US006666.			
PR	22-MAR-2001; 2001US-00816744.			
PR	10-MAY-2001; 2001US-00854208.			
PR	10-MAY-2001; 2001US-00854208.			
PR	25-MAY-2001; 2001WO-US017092.			
XX				
XX	(GETH ) GENENTECH INC.			
XX				
PI	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;			
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;			
XX				
DR	WPI: 2002-404358/43.			
DR	P-PSDB; ADY31902.			
XX				
PT	Isolated nucleic acid useful in a method for stimulating the			
PT	proliferation, gene expression or differentiation of cells and in			
PT	detecting the presence of a tumor.			
XX				
PS	Claim 2; SEQ ID NO 161; 296pp; English.			
XX				
CC	The invention relates to human PRO polypeptides (secreted and			
CC	transmembrane polypeptides) and the PRO polynucleotides encoding them.			
CC	The PRO polypeptides and polynucleotides are useful as pharmaceuticals,			
CC	diagnostics, biosensors or bioreactors. They are particularly useful for			
CC	detecting tumours (e.g. lung tumour, colon tumour, breast tumour,			
CC	prostate tumour, rectal tumour or liver tumour) in a mammal, for			
CC	stimulating the release of tumour necrosis factor (TNF)-alpha from human			
CC	blood, for stimulating the proliferation or differentiation of			
CC	chondrocyte cells, for stimulating the proliferation of or gene			
CC	expression in pericyte cells or for stimulating the proliferation of			
CC	normal human dermal fibroblasts. The PRO nucleic acids are useful as			
CC	hybridisation probes, in chromosome and gene mapping, in generating			
CC	antisense RNA and DNA, in preparing PRO polypeptides by recombinant			
CC	technology, in generating transgenic animals or knock-out animals which			
CC	may be used in the development and screening of therapeutically useful			
CC	reagents, in gene therapy, in chromosome identification, as chromosome			
CC	markers and in generating probes. The PRO polypeptides, or anti-PRO			
CC	antibodies, are useful for preparing a medicament for treating a			
CC	condition which is responsive to the PRO polypeptides or anti-PRO			
CC	antibodies, such as pericyte-associated tumours and bone and/or cartilage			
CC	disorders (e.g. arthritis, sports injuries), involving inducing the re-			
CC	differentiation of chondrocytes. The PRO polypeptides are useful as			
CC	molecular markers for protein electrophoresis, and in tissue typing. This			
CC	sequence represents a human PRO polynucleotide of the invention. Note:			

CC The sequence data for this patent is also available in electronic format  
CC from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 1587 BP; 331 A; 490 C; 432 G; 334 T; 0 U; 0 Other;

Query Match 98.7%; Score 1579.4; DB 7; Length 1587;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	20	CAGCCACAGAGGTCATGACGGGTATTAATCTGCTGGCCCTCTGGGGTTCACTCTCCC	79
Db	1	CAGCCACAGAGGTCATGACGGGTATTAATCTGCTGGCCCTCTGGGGTTCACTCTCCC	60
Qy	80	ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGT	139
Db	61	ACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGT	120
Qy	140	GTCCGACCTGCCCGCAATGGAACCCCTAAGAACACCAAGTTCGACAGCGCTTTGGGGTG	199
Db	121	GTCCGACCTACCCCGCAATGGAACCCCTAAGAACACCAAGTTCGACAGCGCTTTGGGGTG	180
Qy	200	CCAGGACACCTTGATGCTCATTTAGAGCGGACCCCAAGTGAAGCTGTGCTCTCCAAGGG	259
Db	181	CCAGGACACCTTGATGCTCATTTAGAGCGGACCCCAAGTGAAGCTGTGCTCTCCAAGGG	240
Qy	260	CTGCAGGAGGCCAAGGACAGGAGCCCGCTCACTGAGCACCGGATGGCCCGGCGCT	319
Db	241	CTGCAGGAGGCCAAGGACAGGAGCCCGGCTCACTGAGCACCGGATGGCCCGGCGCT	300
Qy	320	CTCCCTGATCTCTACACCTTCTGTGCGCGCAGGAGGACTTCTGCAACCAACCTCGTTAA	379
Db	301	CTCCCTGATCTCTACACCTTCTGTGCGCGCAGGAGGACTTCTGCAACCAACCTCGTTAA	360
Qy	380	CTCCCTCCCGTTTGGGCCCCACAGCCCCCAGCAGACCCAGATTCCTTGAAGTGGCCAGT	439
Db	361	CTCCCTCCCGTTTGGGCCCCACAGCCCCCAGCAGACCCAGATTCCTTGAAGTGGCCAGT	420
Qy	440	CTGCTTCTCATGAAGGCTGTCTGGAGGGGACCAACAGAGAGATCTGCCCAAGGGGAC	499
Db	421	CTGCTTCTCATGAAGGCTGTCTGGAGGGGACCAACAGAGAGATCTGCCCAAGGGGAC	480
Qy	500	CACACACTGTTATGATGGCTCTCAGGCTCAGGGGAGGAGGACTTCTTCCCAATCTGAG	559
Db	481	CACACACTGTTATGATGGCTCTCAGGCTCAGGGGAGGAGGACTTCTTCCCAATCTGAG	540
Qy	560	AGTCCAGGATGATGCCCGCCAGCAGGTTCGCTCAATGGGACACAGGAAATTTGG	619
Db	541	AGTCCAGGATGATGCCCGCCAGCAGGTTCGCTCAATGGGACACAGGAAATTTGG	600
Qy	620	GCCCGTGGTATGATGAGGACTGCAATAGGAAGATTTCTGACCTGTCTATCGGGGAC	679
Db	601	GCCCGTGGTATGATGAGGACTGCAATAGGAAGATTTCTGACCTGTCTATCGGGGAC	660
Qy	680	CACCATTTATGACACACCGAACTTGGCTCAAGAACCCACTGATTGGACCATCGAATAC	739
Db	661	CACCATTTATGACACACCGAACTTGGCTCAAGAACCCACTGATTGGACCATCGAATAC	720
Qy	740	CGAGATGTGAGGTGGGGCAGGTGTGCTCAGGAGACGCTGCTGCTCATAGATGTAGGACT	799
Db	721	CGAGATGTGAGGTGGGGCAGGTGTGCTCAGGAGACGCTGCTGCTCATAGATGTAGGACT	780
Qy	800	CACATCAACCTCGTGGGGACAAAGGCTGCAGGACTGTGGGGCTCAAAATTTCCAGAA	859
Db	781	CACATCAACCTCGTGGGGACAAAGGCTGCAGGACTGTGGGGCTCAAAATTTCCAGAA	840
Qy	860	GACCACCATCACTCAGCCCTCTCTGGGGTGTGTGGGCTCTCTATACCCACTTCTGCTC	919
Db	841	GACCACCATCACTCAGCCCTCTCTGGGGTGTGTGGGCTCTCTATACCCACTTCTGCTC	900
Qy	920	CTCGGACCTGTGCAATAGTCCAGCAGCAGCGGTTCTGCTGAACCTCCCTCCCTCTCA	979
Db	901	CTCGGACCTGTGCAATAGTCCAGCAGCAGCGGTTCTGCTGAACCTCCCTCCCTCTCA	960

Qy	980	AGCTGCCCTGTCTCCAGAGACCGGACGCTCTACCTGTGTGAGCCCTTTGGAACCTG	1039
Db	961	AGCTGCCCTGTCTCCAGAGACCGGACGCTCTACCTGTGTGAGCCCTTTGGAACCTG	1020
Qy	1040	TTCAAGTGGCTTCCCGGAAATGACCTGCCCGAGGGGCGCCACTCATTTGTTATGATGGTA	1099
Db	1021	TTCAAGTGGCTTCCCGGAAATGACCTGCCCGAGGGGCGCCACTCATTTGTTATGATGGTA	1080
Qy	1100	CATTCACTCTCAGGAGGTGGCTGCACCAAAATGAGCAATCAGGGCTCGTGGCCCA	1159
Db	1081	CATTCACTCTCAGGAGGTGGCTGCACCAAAATGAGCAATCAGGGCTCGTGGCCCA	1140
Qy	1160	ACCTTCCAGCTTCTTTTGAACACACACAGCAAAATCGGATCTTCTCGCGCGTGAGAA	1219
Db	1141	ACCTTCCAGCTTCTTTTGAACACACACAGCAAAATCGGATCTTCTCGCGCGTGAGAA	1200
Qy	1220	GGGTGATGTGAGCCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCCTTGAGTGC	1279
Db	1201	GGGTGATGTGAGCCTCTGCTCTCAGCATGAGGAGGTGGGCTGAGGGCCTTGAGTGC	1260
Qy	1280	TCTCACTTGGGGGTGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	1339
Db	1261	TCTCACTTGGGGGTGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	1320
Qy	1340	TTCTGCTAACTCTATTACCCCGACGATTTCTTACCGCTGCTGACCCACCTCAAC	1399
Db	1321	TTCTGCTAACTCTATTACCCCGACGATTTCTTACCGCTGCTGACCCACCTCAAC	1380
Qy	1400	TCCCTCTGACCTCATAACTTAATGGCCCTTGGACACCAAGATTTCTTCCCATCTGTCCATG	1459
Db	1381	TCCCTCTGACCTCATAACTTAATGGCCCTTGGACACCAAGATTTCTTCCCATCTGTCCATG	1440
Qy	1460	AATCATCTTCCCGACACACAAATCATTTCAATCTACTACCTAACAGCAACACTGGGGAGA	1519
Db	1441	AATCATCTTCCCGACACACAAATCATTTCAATCTACTACCTAACAGCAACACTGGGGAGA	1500
Qy	1520	GCCTGGAGCATCCGAGCTTGCCTTATGGGAGGGGAGCGCTGGAGGAGTGGCTGCATGTA	1579
Db	1501	GCCTGGAGCATCCGAGCTTGCCTTATGGGAGGGGAGCGCTGGAGGAGTGGCTGCATGTA	1560
Qy	1580	TCTGATTAATACAGACCTCTGTC	1600
Db	1561	TCTGATTAATACAGACCTCTGTC	1581

Search completed: July 11, 2006, 10:47:21  
Job time : 1054 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 11, 2006, 09:31:52 ; Search time 21 Seconds  
(without alignments)  
558.362 Million cell updates/sec

Title: US-10-727-619-2

Perfect score: 2381

Sequence: 1 MSALLLALLGFLPLPGVQ.....WGVLALPALMNGVVCPC 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pap:\*
- 2: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pap:\*
- 3: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pap:\*
- 4: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pap:\*
- 5: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap:\*
- 6: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pap:\*
- 7: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pap:\*
- 8: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	6.7	28	7	US-11-134-871-3056
2	136	5.7	5738	6	US-10-505-928-150
3	131.5	5.5	1450	7	US-11-217-997-6
4	123	5.2	721	7	US-11-175-714-7
5	122	5.1	1464	7	US-11-174-307B-2038
6	121.5	5.1	1418	7	US-11-217-997-38
7	120.5	5.1	1019	7	US-11-174-307B-334
8	120	5.0	1467	7	US-11-174-307B-1022
9	118.5	5.0	5179	7	US-11-105-233-185
10	118	5.0	251	6	US-10-196-749-476
11	118	5.0	810	7	US-11-174-307B-220
12	117.5	4.9	1868	7	US-11-174-307B-2266
13	116	4.9	1505	7	US-11-174-307B-1622
14	115.5	4.9	1547	7	US-11-217-997-22
15	115.5	4.9	1577	7	US-11-217-997-16
16	115.5	4.9	1577	7	US-11-217-997-20
17	115.5	4.9	1598	7	US-11-174-307B-2072
18	115.5	4.9	1620	7	US-11-217-997-42
19	115.5	4.9	1653	7	US-11-217-997-40
20	115	4.8	1502	7	US-11-174-307B-632
21	115	4.8	1594	7	US-11-217-997-18
22	115	4.8	2133	7	US-11-174-307B-894
23	114.5	4.8	864	7	US-11-178-724-27
24	114.5	4.8	1505	7	US-11-174-307B-562
25	114.5	4.8	2003	7	US-11-264-243-8

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26      114      4.8      717      7      US-11-175-714-9      Sequence 9, Appli
27      114      4.8      2124      7      US-11-174-307B-2768      Sequence 2768, Ap
28      114      4.8      2556      7      US-11-071-796A-22      Sequence 22, Appl
29      113.5      4.8      970      7      US-11-174-307B-2336      Sequence 2336, Ap
30      113.5      4.8      1131      7      US-11-174-307B-2558      Sequence 2558, Ap
31      113.5      4.8      1298      7      US-11-174-307B-2774      Sequence 2774, Ap
32      113.5      4.8      1363      7      US-11-174-307B-358      Sequence 358, App
33      113.5      4.8      1363      7      US-11-174-307B-2430      Sequence 2430, Ap
34      113.5      4.8      1484      7      US-11-174-307B-424      Sequence 424, App
35      113.5      4.8      1700      7      US-11-174-307B-1010      Sequence 1010, Ap
36      113.5      4.8      1701      7      US-11-174-307B-2440      Sequence 2440, Ap
37      113      4.7      1493      7      US-11-174-307B-4196      Sequence 4196, Ap
38      112.5      4.7      1861      7      US-11-174-307B-2454      Sequence 2454, Ap
39      111.5      4.7      1422      7      US-11-174-307B-690      Sequence 690, App
40      111.5      4.7      1708      7      US-11-174-307B-2136      Sequence 2136, Ap
41      111.5      4.7      1953      7      US-11-264-243-16      Sequence 16, Appl
42      111.5      4.7      2616      7      US-11-174-307B-1680      Sequence 1680, Ap
43      111      4.7      729      7      US-11-175-714-8      Sequence 8, Appli
44      110      4.6      1315      7      US-11-174-307B-610      Sequence 610, App
45      110      4.6      1685      7      US-11-174-307B-2212      Sequence 2212, Ap

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#### ALIGNMENTS

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RESULT 1
US-11-134-871-3056
; Sequence 3056, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; CURRENT APPLICATION NUMBER: US/11/134,871
; FILE REFERENCE: 66661-116
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3056
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3056

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Query Match      6.7%; Score 159; DB 7; Length 28;
Best Local Similarity 100.0%; Pred.No. 2.3e-07;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      180  MPOPGCNLLNGTQIEIGPVGMTENCNRKD 207
          |||||
Db       1  MPOPGCNLLNGTQIEIGPVGMTENCNRKD 28

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```

RESULT 2
US-10-505-928-150
; Sequence 150, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 150
; LENGTH: 5738
; TYPE: PRT

```

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; ORGANISM: Homo sapiens
US-10-505-928-150

Query Match          5.7%; Score 136; DB 6; Length 5738;
Best Local Similarity 21.4%; Pred. No. 0.011;
Matches 111; Conservative 33; Mismatches 171; Indels 204; Gaps 31;

QY 9 LLGFLPLPGVQ-----ALLCQFTVQ-----HVMKVSIDLPRWTPKNTSC 49
   ||| |||
Db 3246 LVGEELKWFVSVLLGNCSQVCCKGELLQPGGCPPLCGWSAWS-----SWAPCDRSC 3299
   ||| |||

QY 50 DSGL-----GQDTLMLESQPQSVLSLKSCKTRAKDQ 82
   ||| |||
Db 3300 GSGVRRFRSPNPAAWGAPCEGRQELQGCHTV-----CGTGIAGSLGAGVPPSSSQ 3354
   ||| |||

QY 83 EPRVTEHRCPP-----GLSLISYT-----FVCRQEDFCNNLVNSLPLWAPQPP--ADPG 129
   ||| |||
Db 3355 FCTLRTHGMGPTDHTWGIEVFGWTPMTWSNCSQSCLA---PGGFGMRSRRLCFSPG 3411
   ||| |||

QY 130 SLRCPVCLSMGCLGEGTTES-----ICPKGTHCYDGLLRLRGGGIFSNLRVQGC 179
   ||| |||
Db 3412 DSSCPG-----DATQEPCCSPPIECTGFCAGCT-CPGLF-----LHNASC 3452

QY 180 MP--QPCNLLNGTQIEPGVMTENCNRKDFLTCHRGTTIMTHGN--LAQEPDWTSTNT 235
   ||| |||
Db 3453 LPRSQCPCQLHGQLYASGAMARLDSCNN---CTCVSGKMACTSBRCFVACGSPFTLWSL 3509
   ||| |||

QY 236 EMEVGQVCOETLLLDVGLTSL--VGTKCSTVGAQNSOKTTHSAPPGLVASYTHFC 294
   ||| |||
Db 3510 CSCS-----CNVGIIRRRFRAGTAPPAAFGGAECQGTMEA-----EFC 3547

QY 295 SSDLNSASSSVLLNSLPPQAPVPG---DRCQPTCVQPLGTCSSGSPRMTCPRGATH 350
   ||| |||
Db 3548 -----SLRCPGVPVPCMPRDKQWLDCAGPASCA-----ELSNPRGTNQ 3587

QY 351 -CYDGYIHLSSGGLSTRKMSIOGCVAPSSFL-----NHTRQIGFSAREKRDVQPPASQ 404
   ||| |||
Db 3588 TCH-----PGCHC-PSGMILLVSPRGHPGLG-----ASVQPPVAL 3622

QY 405 HEGGGAEGLESLT-----WGVGLALAPALW--WGVVCPSC 437
   ||| |||
Db 3623 ---PGAIGTGVPGAGGMP-----WGFVSHCSRSC 3650

RESULT 3
US-11-217-997-6
; Sequence 6, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shimkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23

; ORGANISM: Homo sapiens
US-10-505-928-150

Query Match          5.5%; Score 131.5; DB 7; Length 1450;
Best Local Similarity 22.7%; Pred. No. 0.0052;
Matches 116; Conservative 34; Mismatches 212; Indels 149; Gaps 31;

QY 5 LMLALLGFLPL-----PGVQALL-CQFGTV-QHVWKVSDLPROMTPKNTSCDS 51
   ||| |||
Db 884 LCLCEAGYVGRCEQCCQPGHFGCGEQLCCQHGAAACDHVSGACTCPAGW--RGTFCEH 941
   ||| |||

QY 52 -----GLGCQDTLMLESQPQSVLSLKSCKTEAKDQEPRTVHRMGPGLSLSYTFVC 104
   ||| |||
Db 942 ACPAGFGLDCRSACN-CTAGAACDAVNGSCLCPAGRRGPRCAE--TCPAGL-----YGDNC 995
   ||| |||

QY 105 RQEDFCNNLVNSLPL-----WA-----PQPADPGSLRCPVCLSMGCLGEG--- 145
   ||| |||
Db 996 RHSCLCQNGTCDPVSCHCACPEGWAGLACEKCPADVRA-----GCRHSGGCLNGGLCD 1051

QY 146 --TTEBICPKGTT--HCYDGLLRLGGGIFSNLRVQCMPPQPCGNLLNGTQIEIGPVGMTE 201
   ||| |||
Db 1052 PHTGRCLCPAGWAGDKQSPCLR---GWFGCAQHCSCPPGA----- 1091

QY 202 NCRKDFLTCHRGTTIMTHGNLAQEPDWTSTNTM-CEVQGV---CQETLLLDVGLTS 257
   ||| |||
Db 1092 -----ACHVVT-----GACRCPGFTGSGCEQCPGPRYGPQCEQLCGCLNGSGCD 1137

QY 258 TLVGTGKCS--VGAQNSOKTTHSAPPGLVASYTHFCSSDLCSASSSVLLNS--LP 313
   ||| |||
Db 1138 AATGACRCPTGFTGTCNL-----TCPQGRFGNCHVCG---CGQGAACDPVTGTCCLCP 1189

QY 314 PQAAPVPGDRQCP-----TC-VQPLGTSSGSPRMTCPRGAT--HC-----Y 352
   ||| |||
Db 1190 PGRAGVRCERGCPCQNRFGVGCETHCTSCRNGGLCHASNGSCSGLGTGRHCELACPPGRY 1249

QY 353 DGYIHL--SGGGLSTKMSIOG-CVAQPSFLLNHTRQIGIFSAREKRDVQPPASQHEGGG 409
   ||| |||
Db 1250 GAACHLECSCHNNSTGEPTATGTCRCGEG-----FYGOACEHPCPGP--FHGAG 1295
   ||| |||

QY 410 AEGLESITWGV-----GLALAPALMWGVVC 434
   ||| |||
Db 1296 CQGLWCQHGAPCDPISGRCLCPAGFHGHFC 1326

RESULT 4
US-11-175-714-7
; Sequence 7, Application US/11175714
; Publication No. US20060122373A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; APPLICANT: Busfield, Samantha J.
```



QY 393 REKRDVQPASQHEGGAGLESLT-----WGVLALAPALMWGVCPS 437  
Db 616 -----ATAAGAGGAGTAATACTATTTCATCGCAGGTGGCATAGCTGGTGAGC 662

## RESULT 6

US-11-217-997-38  
; Sequence 38, Application US/11217997  
; Publication No. US2006011561A1  
; GENERAL INFORMATION:  
; APPLICANT: Valerie L. Gerlach  
; APPLICANT: Elma R. Fernandes  
; APPLICANT: Richard A. Shinkets  
; APPLICANT: Meera Patturajan  
; APPLICANT: Vladimir Y. Gusev  
; APPLICANT: Stacie (Casman) Navara  
; APPLICANT: Velizar T. Tchernev  
; APPLICANT: David W. Anderson  
; APPLICANT: Xiaojia (Sasha) Guo  
; APPLICANT: Luca Rastelli  
; APPLICANT: Mei Zhong  
; APPLICANT: Muralidhara Padigaru  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY  
; FILE REFERENCE: Cura 551 CIP  
; CURRENT APPLICATION NUMBER: US/11/217,997  
; CURRENT FILING DATE: 2005-08-31  
; PRIOR APPLICATION NUMBER: 10/453,372  
; PRIOR FILING DATE: 2003-06-03  
; PRIOR APPLICATION NUMBER: 10/055,877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,478  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/263,351  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/272,870  
; PRIOR FILING DATE: 2001-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-217-997-38

Query Match 5.1%; Score 121.5; DB 7; Length 1418;  
Best Local Similarity 23.1%; Pred. No. 0.035;  
Matches 126; Conservative 33; Mismatches 185; Indels 201; Gaps 37;  
QY 5 LLLALLQLFILPL-----PGVQALL-CQFGTV-QHWVKVSDLPQWTPKNTSCDS 51  
Db 892 LCLCEAGYVGRCEQPCQGHFGGCEQLCCQGHGACDVSGACTCPAGM--RGTFCEH 949  
QY 52 -----GLCQDPTMLIESGPQSVLSKGTCTEAKDQEBRVTEH-----RMGPGLSLI 98  
Db 950 ACPAGFFGLDCRSACN-CTAGAACDAVNGSLCPAGRRGRCAEKCILPRDVRAG-----1002  
QY 99 SYTFVCRQEDFCNNLVNSLPWAPPPADP--GSLRCPV-----CLSMGECLEGTTEEI 150  
Db 1003 -----CRHSGGLN--GGL-----CDPHTGRCLCPAGWTGDKCOS--PCLRGWGEA 1045  
QY 151 C-----PKGTHCYDGLLRLLRGGGIFSNLRVQGCMP-----QPGCNLLNGTQIEG-----195

Db 1046 CAQRCSPPGAACHVVTGACRCPPPGFTGSGCE--QGCPPGRYGPCEQLCGCLNGGSCDAA 1104  
QY 196 -----PVG-MTENCNRKDFLTCHRG-----TTIMTHG-NLAQEPDWTTSNTEMCV 241  
Db 1105 TGACRCPTGLGTDCN-----LTCPPGRFNPCHVCGCGGAACDP-----VTGTCICPPG 1156  
QY 242 QV-----CQETILLIDVGLTSLVGTGKGVSTVGAQNSQKTTIHSAPGV 285  
Db 1157 RAGVRCERCPCPNRFGVGCETCSNRNGLCHASNGSCS--GLGWTGRHCELACPPGR 1213  
QY 286 LVASYTHFCS-----SDLCNSASSSVLLNLPPOAAPVGDRCPT-----CVQPLTCS 336  
Db 1214 YGAAACHLECSCHNNSTCEPATGTGTCRCGPGFYGACBHP-----CPGPHGAGC-QGLCMCQ 1268  
QY 337 SGSP-----RMTCPRGATHCYDGYIHLSCGGLSTRMSIQGCVAAQSPSSFLNHNTRQIGIF 390  
Db 1269 HGAPCDPISGRCLCPAG-----FHGH-----FCERGC--EPGSF-----1300  
QY 391 SAREKRDVQPASQHEG-----GGAEGLESITWGVGLALAPALMWGVVC-----434  
Db 1301 -----GEGHQRCDGAP--CDPVT---GLCLCPPGRSGATCNLDCCRGO 1342  
QY 435 --PSC 437  
Db 1343 FGPSC 1347

## RESULT 7

US-11-174-307B-334  
; Sequence 334, Application US/11174307B  
; Publication No. US20060143729A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS  
; FILE REFERENCE: 2750-1601PUS2  
; CURRENT APPLICATION NUMBER: US/11/174,307B  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/583,671  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,781  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,651  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 5544  
; SEQ ID NO 334  
; LENGTH: 1019  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: Pfam Name: Man-6-P\_recep; Pfam Description: Cation-dependent  
US-11-174-307B-334

Query Match 5.1%; Score 120.5; DB 7; Length 1019;  
Best Local Similarity 24.6%; Pred. No. 0.029;  
Matches 68; Conservative 13; Mismatches 140; Indels 55; Gaps 12;  
QY 133 CPVCLSMGECLEGTTEICP-----KGTTHCYDGLLRGGGIFSNLRVQGCMPQPGCNL 187  
Db 438 CATCT--GCCGGTGTGCAGTAGCTATATCCGCCCATAG-----TAGTGATGGGCT- 489  
QY 188 LNTQIEIGPVGMTECNKRDKFLT-----CHRGTTIMTHGNLAQEPDWTTSNTEMC 238  
Db 490 -GGTTTAGTACCTTACTAATCATTTCTTGCTGTGGAGCTTATCTGGTGGTG--546  
QY 239 EVGVQCEI-----LLLIDVGLTSLVGTGKGVSTVGAQNSQKTTIHSAPGV 285  
Db 547 --GTGCAGTATATCGGTATTTCTCCCTTGGAAATTCGTGGCATAGATGTAATCCCAATG- 603

```
Qy 286 LVASYTHFCSSDLNCSASSSSVLLNSLPQAAAPVPGDRQCPTCVQPLG-TCSSGSPRMT 344
Db 604 -TGGATTACTGGGCCACTGTACTCTCACAGTATACAG-AGCTTTTGGCTCACTATTTC 661
Qy 345 PRGATHCYDGYIHLSGGG-----LSTKMSIQGCV 374
Db 662 AAGATTCCGG-----GGGTCTAGTCGTCGTCAGCAA 692

RESULT 8
US-11-174-307B-1022
; Sequence 1022, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1022
; LENGTH: 1467
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Aa_trans; Pfam Description: Transmembrane amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 34912776; NR Description: P0407B12.25 [Oryza
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21554158; NR Description: amino acid permease-like
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 22136372; NR Description: amino acid permease-like
; OTHER INFORMATION: protein [Arabidopsis thaliana] >gi|20466438|gb|AAM20536.1| amino
; OTHER INFORMATION: acid permease-like protein [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|18422139|ref|NP_568597.1| amino acid transporter family prote
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 10177364; NR Description: amino acid permease-like
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50932903; NR Description: putative amino acid
; OTHER INFORMATION: transporter family II [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|48475084|gb|AAT44153.1| putative amino acid transporter famil
US-11-174-307B-1022

Query Match 5.0%; Score 120; DB 7; Length 1467;
Best Local Similarity 21.6%; Pred. No. 0.049;
Matches 74; Conservative 16; Mismatches 136; Indels 116; Gaps 14;

Qy 129 GSLRCPVC--LSMGGCILE--GTTTEICPKGTHCYDGLRLRGGGIFSNLRVQCMQPQ 184
Db 554 GTCTGCTCTCTCAGCTAGGATATACT--TTCTCGTCGTCGTTGGG-----G 597
Qy 185 CNLLNGTQIEIGPVGWTENCNRKDFLTCHR-----GTTIMTHGNLAQE-----PT 228
```

```
Db 598 CT--TGT-----ATCAACCTAGGTTTGTGAAAAACGCTCTCTAAACGT 638
Qy 229 DWTSNTMEMCEVQVCOETLLID-----VGLTSTLVGTKCSTVGAQNSOKTHHS 280
Db 639 GAGTATTCTCTAGAGCATTCGGATTAGGGAAGATTTTGTAGTCTTCACATCAATTTTCG 698
Qy 281 APQGVLVASYTHFCSSDLNCSASSSSVLLNSLPQAAAPVPGDRQCPT---CVQPLGTGSS 337
Db 699 AT-----CATAGCTGCTATTTCGG-----AAATGGAATCTTACCCGAAATACAG 743
Qy 338 GSPRMTCPRGAT--HCYDGYIHLSGGGLSTKMSIQGCVQAPSSFLNHTROIIGIFSAREK 395
Db 744 GCAACTCTTGCTCCACCAGCCACAGGGAAGATGTTGAAA-----782
Qy 396 RDVQPPASQHEGGGAEGLESITMGVGLALAPALWMGVVCPSC 437
Db 783 -----GGACTATTGTTGTATAGTGTGATCTTC 812

RESULT 9
US-11-105-233-185
; Sequence 185, Application US/11105233
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Thiagalingam et al
; TITLE OF INVENTION: Differential Expression of Genes in MSI
; TITLE OF INVENTION: Tumors
; FILE REFERENCE: 1657/2001
; CURRENT APPLICATION NUMBER: US/11/105,233
; CURRENT FILING DATE: 2005-04-13
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-233-185

Query Match 5.0%; Score 118.5; DB 7; Length 5179;
Best Local Similarity 20.2%; Pred. No. 0.29; Mismatches 48; Indels 149; Gaps 24;
Matches 81; Conservative 48;

Qy 96 SLISYTFVCRQEDFC-----NNLVNSLPLWAPQ-----PPADPGLRCPVCLS-----138
Db 4733 SLQAYALCAQONICLDWRNHTGACLVCEPSHREYQACGPAAE-----PTCKSSSSQON 4787
Qy 139 -----MEGCLGTTTBEICPKGTHCYDGLRLRGGGIFSNLRVQGC-----MPQ-----182
Db 4788 NTVLVEGC-----FCPEGTMYAPGF-----DVCVKTCGCVGPDNVPREFGEH 4830
Qy 183 -----PCNLLNGTQIEIGPVGWTENCNRKDFLTCH-HERGTTIMTHGNLAQEBTDWTTSYTE 236
Db 4831 FEFDKNCVCLGGS--GIICQPKRCQKQKPVTHCVEDGTVLADEVN-----PAD--TCCNIT 4883
Qy 237 MCEVG-QVCQETLLIDVG--LSTLVGTKCSTVGAQNSOKTHI---SAPPGLVASY 290
Db 4884 VKCNTSLCKEKSPVCEPLGFEVSKMVPGRCCPPWCE--SKGVCVHGNAEQPSVPV--Y 4940
Qy 291 THFCSSDLNCSASSSSVLLNSLPQAAAP-----VPGDRQCPTCVQ-----330
Db 4941 SSKQDCVCTDKVDNNTLLNVIACHTVCNTSCSPGFELMEAPGE--CCKKCEQTHCI1KR 4999
Qy 331 -----PLGTCS-----SGSPRMTCPR--GATHCYDGYIHLSGG 361
Db 5000 PDNQHVILKPFDFKDPKNNCTFFSCVKIHNQLISSVSNNITCFNPFDAISICIPGSIITFMEN 5059
Qy 362 G-----LSTKMSIQGCVQAPSSFLNHN 383
Db 5060 GCCKTCTPRNETRVPCSTVPVTTVEVSAGCT---KTVLMNH 5097

RESULT 10
```

```
US-10-196-749-476
; Sequence 476, Application US/10196749
; Publication No. US2006009486A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 476
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-476

Query Match      5.0%; Score 118; DB 6; Length 251;
Best Local Similarity 25.2%; Pred. No. 0.0087;
Matches 57; Conservative 37; Mismatches 92; Indels 40; Gaps 16;

Qy  4 VLLALIGFILPLPGVALLCQFQVQHVW-----KVSLLPQWTPNTSCDSGLCQD 57
Db  8 VILLCFLGAALCLTGSQALQCY--SFEHTYFPPDLRANKLP-----SISCPH--ECFE 57

Qy  58 TLMIEGSPVSLVL-SKGTEAKDQPRVTEHRMGSLSLISYTFV--CRQEDFCN-NL 113
Db  58 AILSLDTGYRAPVTLVRKGCWTG-----PPAQOTQSNPDALPPDYSVVRGC-TTDKCNHL 112

Qy  114 V--NSLP--LWAPQPPADPGSLRCPVCLSM--EGCLEGTTBEI-CPKGTTHCYDGLLR 166
Db  113 MTHDALPNLSQAPDPPTLSGA-ECVACIGVHDDCAIGRSRRVQCHQDTACFGSGRMT 171

Qy  167 GGGIFSNLRVQGMCPQPGCNLLNTQEIQPGVGMTE-----CNRK 206
Db  172 VGNFSPVPYIRTC-HRPSCTTEGTTSPTWTAIDLQSCCEGVLNCRK 216

RESULT 11
US-11-174-307B-220
; Sequence 220, Application US/11174307B
; Publication No. US20060143729A1
```

```
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 220
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-174-307B-220

Query Match      5.0%; Score 118; DB 7; Length 810;
Best Local Similarity 25.8%; Pred. No. 0.035;
Matches 68; Conservative 14; Mismatches 130; Indels 52; Gaps 13;

Qy  133 CPVCLSMEGCLEGTTEEICP-----KGTTHCYDGLLRG-----GGIFSNLRVQG---CM 180
Db  550 CATCCT--GCCGTTGTGCAGCAGCTATATCCGCCCATAGTAGTGGATGGGCTGTATCT 607

Qy  181 PQPGCNLLNGTQIEIGVGMTECNKRDFLTCHRGTTIMTHG-----NLAQEPDWTTSNTE 236
Db  608 TGTGC--CTGT-TTGGAGCTT-----ATCTGGTGGTGGTGCAGTATATCGGTATTC 657

Qy  237 MCEVGQVCQETLLLDVGLTSLVGTGKCSVCAQNSQKTTIHSAPPGVLVASVTHFCSS 296
Db  658 TC-----CCTT-----GGARTTCGGCATAGATGTAATCCGA--ATATGGATTACTG 704

Qy  297 DLCSASSSSVLNLSLPPQAPVPGDRQCPTCVPLGTSCSSSPRMTCPRGATHCYDGYI 356
Db  705 GGCCACTGTACTCAGATATACAGAGCTGTTTGGCTCACTATTTTCAAGATTCCGG-- 762

Qy  357 HLSGGGLSTVM-----STGGCVA 374
Db  763 ---GGGTCTATTCTGTCAGCAA 783

RESULT 12
US-11-174-307B-2266
; Sequence 2266, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 2266
; LENGTH: 1868
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Glyco_hydro_17; Pfam Description: Glycosyl
```

FEATURE: NAME/KEY: misc\_feature  
LOCATION: NAME/KEY: misc\_feature  
OTHER INFORMATION: Pfam Name: X8; Pfam Description: X8 domain  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: NAME/KEY: misc\_feature  
OTHER INFORMATION: GI Number: 7270016; NR Description: 1, 3-beta-glucanase-like  
OTHER INFORMATION: protein [Arabidopsis thaliana] >gi|38257777|sp|O9M088|E135\_ARATH  
OTHER INFORMATION: Putative glucan endo-1,3-beta-glucosidase 5 precursor  
OTHER INFORMATION: ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase)  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: NAME/KEY: misc\_feature  
OTHER INFORMATION: GI Number: 23308419; NR Description: At5g58090/k21119\_70  
OTHER INFORMATION: [Arabidopsis thaliana] >gi|16604491|gb|AAL24251.1|  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: NAME/KEY: misc\_feature  
OTHER INFORMATION: GI Number: 9759535; NR Description: glucanase; glucan  
OTHER INFORMATION: endo-1,3-beta-glucosidase [Arabidopsis thaliana]  
OTHER INFORMATION: >gi|38257732|sp|Q93208|E136\_ARATH Putative glucan  
OTHER INFORMATION: endo-1,3-beta-glucosidase 6 precursor ((1->3)-beta-glucan  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: NAME/KEY: misc\_feature  
OTHER INFORMATION: GI Number: 15242078; NR Description: glycosyl hydrolase  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: NAME/KEY: misc\_feature  
OTHER INFORMATION: GI Number: 50921029; NR Description: putative  
OTHER INFORMATION: 1,3-beta-glucanase [Oryza sativa (japonica cultivar-group)]  
OTHER INFORMATION: >gi|30017525|gb|AAP12947.1| putative 1,3-beta-glucanase [Oryza  
US-11-174-307B-2266

Query Match 4.9%; Score 117.5; DB 7; Length 1868;  
Best Local Similarity 24.5%; Pred. No. 0.11;  
Matches 61; Conservative 12; Mismatches 155; Indels 21; Gaps 9;  
Qy 133 CPVCLSMGEGCTTEICPKGTHCYDGLLRG--GGIFSNLRVQGGPQGNL----- 187  
Db 1424 CGCAAAATGTAATC--TTACAGTACC--TCAGTTGGGACC---AAGCGTGAGCTACGCTT 1477  
Qy 188 -LNGTQIGPVGMPENCRKDFLTCHRTTITMTHGNLAQEPDWTNTSEMCEVGQVCQE 246  
Db 1478 GTGATCATGCTGATGC-ACAGTCTTGGTTATGCTCCTCTTGTGTAACCTGAATCTA 1536  
Qy 247 TLLIDVGLTSLVGT-KGCVTGAQNSQKTIHSAPPGVLVASYTHFCSSDLNCSASS 305  
Db 1537 GCACAGAATGTTTCGTATGCGTTCAATAGCTATTACCAGGTAAGTAATCAGCTCGACAGT 1596  
Qy 306 SVLNSLPPQNAAPVPGDRQCPTCVQPLGTCSGSPRMTCPRGATHCYDGYHLSSGGGLST 365  
Db 1597 GCGGTGAAGTTCGCGGGTCTCTCTATAGTACAGTA--CTAGGGAT-CCTTCTGTTGGAGT 1653  
Qy 366 KMSIQGCV 374  
Db 1654 ----TGCAA 1658

RESULT 13  
US-11-174-307B-1622  
Sequence 1622, Application US/11174307B  
Publication No. US20060143729A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai  
APPLICANT: BROVER, Vyacheslav  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS  
FILE REFERENCE: 2750-1601PUS2  
CURRENT APPLICATION NUMBER: US/11/174,307B  
PRIOR FILING DATE: 2005-06-30  
PRIOR APPLICATION NUMBER: 60/583,671

PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/583,781  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/583,651  
PRIOR FILING DATE: 2004-06-30  
NUMBER OF SEQ ID NOS: 5544  
SEQ ID NO 1622  
LENGTH: 1505  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURES:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: GI Number: 34905882; NR Description: P0458E05.17 [Oryza  
OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|21902069|dbj|BAC05617.1|  
US-11-174-307B-1622

Query Match 4.9%; Score 116; DB 7; Length 1505;  
Best Local Similarity 24.2%; Pred. No. 0.11;  
Matches 72; Conservative 17; Mismatches 138; Indels 70; Gaps 14;  
Qy 129 GSLEPCVLSMEGCLGCTTEICPKG-TTHCYDGLLRG--GGIFSNLRVQGG----- 178  
Db 330 GAAACTCTCACTTCCAAATTTCTTAGATTGATTGGTTCTGTGGCTATAGCAGTATCATC 389  
Qy 179 -----CMPQPCNLLNGTQEIPIPGVMTENCNRKDFLTCHRTTITMTHGNLAQEP 227  
Db 390 ATGCTCGCTTCTCTGCTCTGATAAAGCGGCTCTC-AAGTTTATGTTAGTAGTCACCG 448  
Qy 228 TDWT-----TSNTEMCEVGQVCQETLLIDVGLTSLVGTGKGVSTVG-----AQNS 273  
Db 449 TCTTTATCAAGTCTTTAGACTTGAGC-----TTGATAATT--TTGCTTCTGCTTCAACA 499  
Qy 274 QKTIHSAPPGVLVASYTHFCSSDLNCS-----ASSSVLLNSLPPQNAAPVPGD-----RQC 325  
Db 500 TCCTAACATATGTTCAAGCT-TCTTGGCTATTTCGATGATTTCAGAGGAAAATGTTGCTCTTC 558  
Qy 326 PTCVQPLG-----TCSSGSPRMTCPRGATHCYDGYHLSSGGGLSTKMSIQGCV 374  
Db 559 TTTGTGATATCTTCTCAAGGAAATC-----TACAAG-----AGAAGCTCCAAAGCA 607

RESULT 14  
US-11-217-997-22  
Sequence 22, Application US/11217997  
Publication No. US20080111561A1  
GENERAL INFORMATION:  
APPLICANT: Valerie L. Gerlach  
APPLICANT: Elma R. Fernandes  
APPLICANT: Richard A. Shimkets  
APPLICANT: Meera Patturajan  
APPLICANT: Vladimir Y. Gusev  
APPLICANT: Stacie (Casman) Navara  
APPLICANT: Velizar T. Tchernev  
APPLICANT: David W. Anderson  
APPLICANT: Xiaojia (Sasha) Guo  
APPLICANT: Luca Rastelli  
APPLICANT: Mei zhong  
APPLICANT: Muralidhara Padigaru  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY  
FILE REFERENCE: Cura 551 CIP  
CURRENT APPLICATION NUMBER: US/11/217,997  
PRIOR FILING DATE: 2005-08-31  
PRIOR APPLICATION NUMBER: 10/453,372  
PRIOR FILING DATE: 2003-06-03  
PRIOR APPLICATION NUMBER: 10/055,877  
PRIOR FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24



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; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 22
; LENGTH: 1547
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-217-997-22

Query Match          4.9%; Score 115.5; DB 7; Length 1547;
Best Local Similarity 20.6%; Pred. No. 0.12;
Matches 124; Conservative 36; Mismatches 210; Indels 231; Gaps 35;

Qy 17 PGV-QALLCQFGTV-QHVWKVSDLPQWTPKNTSCDS-----GLCQDQTLMLIESGPQ 67
Db 887 PGCEQRCCQGHGAACDHVSGACTCPAGW--RGTFCEHACPAAGFGLDCRSACN-CTAGAA 943
Qy 68 VSLVLSKGCTEAKDQBPVTE-----HR-----MG 92
Db 944 CDVANGSCLCPAGRRGPRCAESACPATYGHNCQAACACFNGASCDPVHGQCHCAPGMWG 1003
Qy 93 P-----GLSLISYTFVCRQEDFCNNLVNSLPL-----WAPQPPADPGSLRCPV 135
Db 1004 PSCLOACPAGL-----YDNCNHSCLCQNGGTCDFVSGHCACPEGWA-----GLACEV 1051
Qy 136 -----CLSMEGCLEG-----TTEICPKGTT-----HCYDGL 162
Db 1052 ECLPRDVRAGCRHSGGCLNGGLCDPHTGRCLCPAGWTGDKQCSPAACAKGTGPHC-EGR 1110
Qy 163 LRLRG-----QETGPGVMTENCNRK-----DFTLCHRGTTIMT-----HGNLAQEPD 191
Db 1111 CACRWGGFCHLATGACLCPPGWRGPHLSAACLRGWFGEACAQRCSCPPGAACHVHTGACR 1170
Qy 192 -----QETGPGVMTENCNRK-----DFTLCHRGTTIMT-----HGNLAQEPD 230
Db 1171 CPGFTSGCEQACPFSGFGEDCAQMCQCPGENPACHPATGTCSCAAGYHGSPCQ----- 1225
Qy 231 TTSNTEMEVQGV---COETLLLDVGLTSTLVTKGCST--VGAQNSQKTTIHSAPGV 285
Db 1226 ---QRCPPGRYFGCEQLCGCLNGGSCDAATGACRCPTFLGTDCLN-----TCPQGR 1275
Qy 286 LVASYTHFCSSDLNCSASSSVILNS--LPQAAAPVPGDRCP-----TC-VQPL 332
Db 1276 FGPNCETHVCG---CGQGAACDPVTGTCCLPPRAGVRCERCGPQNRFGVGCEHTCSCRNG 1332
Qy 333 GTCSSGSPRMTCPRGAT--HC-----YDGYIHL--SGGGLSTKMSIQG--CVAQPSF 379
Db 1333 GLCHASNGSCSLGWTGRHCELACPPGRYGAACHLECSCHNNSTCPATGTCRGGP-- 1390
Qy 380 LLNHTROIIGFSAREKRDVQPPASQHEGGGAEGLESITWGV-----GLALAPALMWGV 433
Db 1391 -----FYQACEHPCCFPF--FHGAGCQGLCWQCQHGAPCDPISGRCLCPAGFHGF 1438
Qy 434 C 434
Db 1439 C 1439

RESULT 15
US-11-217-997-16
; Sequence 16, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shimkets
; APPLICANT: Meera Patturajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Casman) Navara
; APPLICANT: Velizar T. Tchernev
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Rastelli
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 1577
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-217-997-16

Query Match          4.9%; Score 115.5; DB 7; Length 1577;
Best Local Similarity 20.6%; Pred. No. 0.13;
Matches 124; Conservative 36; Mismatches 210; Indels 231; Gaps 35;

Qy 17 PGV-QALLCQFGTV-QHVWKVSDLPQWTPKNTSCDS-----GLCQDQTLMLIESGPQ 67
Db 917 PGCEQRCCQGHGAACDHVSGACTCPAGW--RGTFCEHACPAAGFGLDCRSACN-CTAGAA 973
Qy 68 VSLVLSKGCTEAKDQBPVTE-----HR-----MG 92
Db 974 CDVANGSCLCPAGRRGPRCAESACPATYGHNCQAACACFNGASCDPVHGQCHCAPGMWG 1033
Qy 93 P-----GLSLISYTFVCRQEDFCNNLVNSLPL-----WAPQPPADPGSLRCPV 135
Db 1034 PSCLOACPAGL-----YDNCNHSCLCQNGGTCDFVSGHCACPEGWA-----GLACEV 1081
Qy 136 -----CLSMEGCLEG-----TTEICPKGTT-----HCYDGL 162
Db 1082 ECLPRDVRAGCRHSGGCLNGGLCDPHTGRCLCPAGWTGDKQCSPAACAKGTGPHC-EGR 1140
Qy 163 LRLRG-----QETGPGVMTENCNRK-----DFTLCHRGTTIMT-----HGNLAQEPD 191
Db 1141 CACRWGGFCHLATGACLCPPGWRGPHLSAACLRGWFGEACAQRCSCPPGAACHVHTGACR 1200
Qy 192 -----QETGPGVMTENCNRK-----DFTLCHRGTTIMT-----HGNLAQEPD 230
Db 1201 CPGFTSGCEQACPFSGFGEDCAQMCQCPGENPACHPATGTCSCAAGYHGSPCQ----- 1255
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Qy 231 TTSNTEMCVQV---COETLLIDVGLTSLVGTGCGST--VGAQNSQKTTIHSAPGV 285
Db 1256 -----QRCPPRYGPGCEOLCGCLNGSGCDAATGACRCPTGFLGTDCL-----TCQGR 1305
Qy 286 LVASYTHPCSSDLNCSASSSVLLNS---LPQAAAPVPGDROCP-----TC-VQPL 332
Db 1306 FGPNCTHVCG---CGQGAACDPVTGTCCLPPFRAGVRCERGCPCQNRFGVGCETCSRNG 1362
Qy 333 GTCSSGSPRMTCPRGAT--HC-----YDGYIHL--SGGGLSTKMSIQG-CVAQPSF 379
Db 1363 GLCHASNGSCGLGWTGRHCELACPPGRYGAACHLECSCHNNSTCEPATGTCRCGP-- 1420
Qy 380 LLNHTROIGIFSAREKRDVQPPASQHEGGGAEGLESITWGV-----GLALAPALWGVV 433
Db 1421 -----FYGQACEHPCPPG--FHGAGCGGLCWCQHGAPCDPISGRCLCPAGFHGF 1468
Qy 434 C 434
Db 1469 C 1469

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Search completed: July 11, 2006, 09:35:15  
Job time : 23 secs

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